METHODS TO INHIBIT INFECTIOUS AGENT TRANSMISSION DURING XENOTRANSPLANTATION

Background of the Invention

The success of solid organ transplantation protocols continues to improve while the availability of donor organs remains limited, leading to a critical shortage (Policy et al., 1996). In 1995, only one-half of the patients on organ transplant waiting lists received transplants. Approximately nine patients per day died while waiting for a suitable organ to become available. Xenotransplantation of animal organs is under consideration as a supplemental approach to alleviate this shortage (Policy et al., 1996). The pig is currently the donor of choice for cells, tissues and vascularized organs used in permanent and transient xenotransplantation treatments (Fishman, 1994). Swine offer a number of advantages as a source for xenotransplantations: economic and animal husbandry issues, the ability to produce transgenic animals, experience as a transplantation model, and the development of specific pathogen-free herds to eliminate known pathogens.

Pig to human organ transplants are discordant. However, several groups have engineered transgenic pig lines in efforts to control hyperacute rejection (HAR) (Lin et al., 1996). Two immunologic factors initiate HAR of xenografts: the interaction of natural xenoreactive antibodies to the Galα1-3Gal carbohydrate (α-Gal) of discordant cell proteins; and the inability of the xenograft complement regulatory proteins to control the recipient's complement system. Several approaches to control HAR are being studied including the ablation of Galα1-3Gal expression (Sandrin et al., 1995), and the design of transgenic pigs which express complement regulatory proteins (e.g., DAF, CD59) which have been shown to be protective against HAR (Diamond et al., 1996; Foder et al., 1994; McCurry et al., 1995; Oldham et al., 1996; Ryan, 1995).

Several promising xenotransplantation approaches use pig cells and tissues in protocols where xenotic cells and tissues are not rejected as readily as whole organs: fetal pig neuronal cells producing dopamine have been tested in patients to replace cells destroyed by Parkinson's disease (Deacon et al., 1997);

and fetal pig pancreatic islet cell clusters have been tested in protocols to treat diabetes (Groth et al., 1994). Another xenotransplantation approach has used pig liver and kidney xenografts as temporary support treatments for patients with fulminant organ failure (Breimer et al., 1996; Groth et al., 1994; Makowka et al., 1995). These studies have sparked research in the use of bioartificial organs and whole organ perfusion using xenogeneic tissue for bridging patients prior to transplantation. The early successes of these innovative clinical approaches indicate that xenotransplantation protocols using pig cells, tissues and organs will continue regardless of the results of solid organ xenotransplantation.

Besides the expected immunological hurdles that must be overcome, xenotransplantation produces a risk of transmitting infectious disease (xenoses) from the source animal tissue to the recipient, and possibly to the recipient's contacts. Xenotransplantation increases the risk of transferring infectious agents from pigs to humans due to the breach of the normal physical barriers against infectious agents upon introduction of pig cells, tissues or organs; the therapeutic immunosuppression of the recipient to prevent graft rejection which interferes with the mechanisms which defend human cells from infection by zoonotic viruses; and the genetic modifications of pigs, e.g., those being tested to control HAR or modify complement activation, may allow zoonotic viruses to evade immune surveillance or prevent the inactivation of invading enveloped viruses (Bergelson et al., 1995; Dorig et al., 1993; Fishman, 1994; Ward et al., 1994; Weiss, 1998).

Since most vertebrates carry endogenous retroviruses in their germline DNA (Boeke et al., 1997), endogenous retroviruses in xenografts may be an infectious risk to xenotransplant patients. The risks of transmission to humans with endogenous viruses of non-humans are unknown and difficult to assess. Endogenous retroviruses from a variety of animals, including baboons, cats, and mice, can infect human cells (Boeke et al., 1997). The ability of endogenous murine leukemia viruses (MLVs) to be activated and infect human tumor xenografts in immunodeficient mice is well documented (Achong et al., 1976; Beattie et al., 1982; Crawford et al., 1979; Gautsch et al., 1980; Suzuki et al., 1977; Tralka et al., 1983; Wunderi et al., 1979). The observation that the gibbon ape leukemia virus SEATO, a virus most likely derived from an endogenous

retrovirus of Asian wild mice, can cause chronic myelogenous leukemia in normal juvenile gibbon apes highlights the potential risks of exposure to xenotic endogenous retroviruses (Kawakami et al., 1980; Lieber et al., 1975).

There have been several reports of MLV retroviral vector stocks that contain the result from recombination between the vector and endogenous retroviruses in the genome of the helper cell line (Chong et al., 1998; Donahue et al., 1992; Patience et al., 1996; Purcell et al., 1996; Vanin et al., 1994). In one study, 3 of 10 rhesus monkeys developed T-cell lymphomas after autologous transplantation of enriched bone marrow stem cells transduced with a MLV retroviral vector stock containing an array of MLV-related recombinant viruses (Vanin et al., 1994). Finally, the activation of endogenous retrovirus by human tumor xenografts as well as studies of graft versus host reaction *in vivo* and mixed lymphocyte reaction *in vitro* (Hirsch et al., 1970; Hirsch et al., 1972; Levy et al., 1977; Sherr et al., 1974), demonstrate that normally inactive endogenous retroviruses can be induced by xenotransplantation conditions.

Pig endogenous retroviruses (PERVs) released by established pig cell lines were observed in the 1970s, but the host range of these viruses was thought to be restricted to pig cells (Armstrong et al., 1971; Lieber et al., 1975; Moennig et al., 1974; Strandstrom et al., 1974; Todaro et al., 1974). Recently, replication-competent pig endogenous retroviruses (PERV) were identified, and shown to be capable of productively infecting human cells *in vitro* (Wilson et al., 1998; Martin et al., 1998; Patience et al., 1997; Takeuchi et al., 1997; Weiss, 1997). PERVs have been associated with pig lymphomas (Bostock et al., 1973; Frazier, 1985; Moennig et al., 1974; Strandstrom et al., 1974; Suzuka et al., 1985). Although Heneine et al. (1998) and Patience et al. (1998) screened blood lymphocytes and sera from 10 diabetic patients that received porcine fetal islet cells, and 2 renal dialysis patients whose circulation had been linked with pig kidneys extracorporeally, respectively, neither group detected PERVs. However, the risk of viral infection is increased in transplantation by the presence of factors commonly associated with viral activation, e.g., immune suppression, graft-versus-host disease, graft rejection, viral coinfection and cytotoxic therapies. Thus, in immunosuppressed xenotransplant patients, there may be a greater risk that infection would lead to disease.

Therefore, there is a need for a method to inhibit or prevent transmission of infectious agents, from donor to recipient and/or recipient to donor, after cell, tissue or organ transplant.

Summary of the Invention

The invention provides isolated and purified nucleic acid molecules and methods useful to inhibit or prevent the transmission of an infectious agent during xenogeneic or allogeneic cell, tissue or organ transplant. Infectious agents include, but are not limited to, viruses, bacteria and parasites. The invention includes prophylactic and therapeutic uses of the nucleic acid molecule of the invention which encodes at least a portion of a polypeptide of the infectious agent or which encodes at least a portion of the receptor employed by the infectious agent to enter the cells of the transplant recipient. It is preferred that the expression of the nucleic acid molecule in a donor cell, tissue or organ inhibits or prevents the transmission of the infectious agent from the donor cells, tissue or organ to a transplant recipient, or, alternatively, the transmission of the infectious agent from the recipient to the donor cell, tissue or organ. Preferred transplant recipients are mammals such as primates, e.g., humans, apes and monkeys, as well as canines, felines, bovines, ovines, swine, and equines.

Preferably, the transmission of the following infectious agents is inhibited or prevented: retroviruses, lentiviruses, herpesvirus, e.g., cytomegalovirus (CMV) and Epstein Barr virus (EBV), and hepatitis viruses, e.g., hepatitis A, B or C. Thus, transplanted organs, e.g., bioengineered organs, tissues, or cells, e.g., stem cells, including allografts, e.g., human-to-human transplants, or xenografts, are genetically modified to inhibit the infection of several major infectious pathogens that limit the success of transplantation (e.g., CMV, EBV, HIV and hepatitis viruses) or the infection by potential pathogens, e.g., endogenous viruses such as PERVs. Preferred nucleic acid molecules useful in the practice of the invention include a nucleic acid molecule which encodes gag, pol, env, protease, and accessory proteins (e.g., Vpr, Vif, Nef, Tat, or Rev) of retroviruses, lentiviruses and spumaviruses; a nucleic acid molecule which comprises a capsid or envelope gene of a herpesviruses, e.g., HSV 1 and 2, EBV and CMV; a nucleic acid molecule which comprises the C gene (nucleocapsid), ORFS/pre-S gene (viral surface glycoproteins), ORFX gene

(regulatory protein), or ORFP gene (viral polymerase) of Hepadnaviruses, e.g., hepatitis B virus; a nucleic acid molecule which comprises the C gene (viral capsid) or the E1 and/or E2 gene of Flaviviruses, e.g., hepatitis C virus; a nucleic acid molecule which comprises ORF1, e.g., which encodes Pro (protease), the X gene, the H gene (helicase), the Pol gene (polymerase), or the ORF2 gene, which codes for capsid, of hepatitis E virus; and a nucleic acid molecule which encodes the P1 gene, the 1A gene, the 1B gene, the 1C gene, or the 1D gene (capsid and glycoproteins) of hepatitis A virus. The alteration of human cells and tissue is preferred for modifying pluripotential cells and in *ex vivo* gene therapy protocols.

Preferably, viral entry and/or assembly is inhibited. To inhibit viral entry, receptor interference may be employed. Receptor interference refers to the expression of a receptor protein for the infectious agent or the ligand thereof, e.g., a viral ligand such as a viral glycoprotein. Preferably, the genome of the donor cell, tissue or organ is augmented with DNA encoding the viral ligand thereby preventing infection. Alternatively, or in addition, capsid-targeted viral inactivation may be employed to inhibit or prevent viral replication. Capsid-targeted viral inactivation (CTVI), reduces or eliminates the production of infectious virus by incorporating a degradative enzyme into newly synthesized viral particles, e.g., by expressing a fusion polypeptide comprising a viral polypeptide and a degradative enzyme. Degradative enzymes such as nucleases, e.g., RNase H, staphylococcal nuclease or ribozymes (see Marshall et al., 1994, and U.S. Patent No. 5,811,275), lipases or proteases, may be employed in the practice of the invention. Preferred fusion polypeptides include fusions of viral capsid, envelope or accessory proteins such as Vif, Vpx, Vpr and Nef, with degradative enzymes.

A preferred xenograft for use in the methods of the invention is swine neuronal cells, pancreatic islet cells, hepatocytes, heart, liver or kidney. Therefore, the invention provides a method in which the genomic DNA of swine cells, tissue or organ to be transplanted is augmented with a recombinant DNA molecule encoding a polypeptide of an infectious agent which binds to a cell surface receptor of a transplant recipient, e.g., a viral glycoprotein, or a fusion polypeptide comprising at least a portion of an infectious agent polypeptide and

a degradative enzyme. Infectious agents in this embodiment of the invention include, but are not limited to, those described in Table 1 of Fishman (1994), which is specifically incorporated by reference herein. In particular, PERVs are useful in CTVI methods to inhibit or prevent human-tropic PERV infection in xenotransplant patients.

As described hereinbelow, human tropic PERVs are produced by activated peripheral blood mononuclear cells. The relative PERV proviral copy number doubled upon passaging of the 1°-293 PERV-infected cells to fresh 293 cells, indicating that passaging the virus may amplify the replication-competent PERV. Only PERV-A *env* sequences were detected in DNA isolated from all three 293/PERV infected cultures by PCR analysis with PERV-A, PERV-B and PERV-C specific *env* primers. The 1°-293/PERV DNA contained a low level of PERV-C *env*. PERV-B *env* was not detected in any culture. Characterization of these PERVs indicated that human-tropic PERVs may be more diverse than previously thought. For example, significant sequence differences were found in the cloned LTR and *env* sequences compared to known PERV sequences. The 293/PERV LTRs contained 71 additional nucleotides compared to the PERV-MSL LTR, and the envelope amino acid sequence contains a PERV-A surface region (SU) sequence but a PERV-C transmembrane (TM) region. These PERVs are useful to determine the tissue tropism of various isolates and to determine the prevalence of anti-PERV antibodies in humans exposed to sources of PERV, e.g., pig slaughterhouse workers and xenotransplant patients such as those having a bioartificial liver with pig hepatocytes, as well as in the methods of the invention.

Thus, a vector comprising a nucleic acid molecule of the invention may also be employed to deliver soluble *env* genes to mammalian donor cells, tissues or organs prior to cell, tissue or organ transplantation so that the transplanted cells, tissues or organs are less susceptible to infection by an infectious agent, the genome of which comprises the *env* gene. For example, soluble PERV *env* genes are introduced to donor swine cells, tissues or organs to inhibit infection of the cells, tissues or organs by PERV, e.g., to inhibit infection by PERVs after the virus is reactivated following transplantation.

As also described hereinbelow, two genes encoding an avian leukosis virus (ALV) receptor protein, sTva proteins, *stva* and *stva-mIgG*, were efficiently delivered and broadly expressed by ALV-based retroviral vectors both in cultured cells and in chickens. Both the sTva and sTva-mIgG proteins significantly inhibited ALV(A) infection *in vitro* and *in vivo*. The antiviral effect was specific for ALV(A), consistent with a receptor interference mechanism.

Brief Description of the Figures

Figure 1. Stimulated pig peripheral blood mononuclear cells (PBMCs) produce replication-competent human-tropic PERV. (A) Porcine PBMC were cultured with either phytohemagglutinin (PHA) + phorbol myristate acetate (PMA) (black bars) or PMA + calcium ionophore (grey bars) and the supernatants assayed for RT activity. (B) NIH and Yucatan minipig PBMC stimulated by PHA + PMA were cocultured with ST-IOWA cells. Cell culture supernatants were assayed for RT activity. Background RT values for uninfected ST-IOWA cells have been subtracted from the values shown. NIH (black squares); Yucatan (open circles). (C) NIH minipig PBMC stimulated with PHA + PMA were cocultured with human 293 cells: 293 cells cocultured with live PBMC (closed squares); with lethally irradiated PBMC (open squares). The cell culture supernatants were assayed for RT activity.

Figure 2. Schematic overview of the generation of the human 293 cell cultures infected with PERV produced by stimulated NIH minipig primary PBMC.

Figure 3. Relative titers of PERV produced from the infected 293 cell cultures. The titer of MLV-βgal/PERV pseudotyped virus stocks produced from the 1°, 2° and 3°-293/PERV cultures were quantitated on human 293 cells (open bars) and pig ST-IOWA cells (black bars). The assays scored β-galactosidase producing cells (BFU) and were done in triplicate.

Figure 4. Analysis of the relative number of PERV proviruses per cell in the 293/PERV infected cultures. Genomic DNA isolated from human 293 cells and the 293/PERV infected cultures was digested with EcoRI, and the fragments separated by agarose gel electrophoresis, transferred to nitrocellulose, and probed with ^{32}P-labeled PERV *pol* sequences. Two internal proviral DNA fragments hybridized to the PERV *pol* probe as expected. The film was scanned

and the bands quantitated by Image Quant (Molecular Dynamics, Sunnyvale, CA). The blot was stripped and reprobed with ^{32}P-labeled human GAPDH sequences to normalize for the amount of DNA loaded per lane. After the band densities were normalized, the PERV *pol* level of the 1°-293/PERV DNA was set as 1 copy.

Figure 5. RT activity observed in cocultures of 293/2° virus producer cells and human hematopoietic cell lines. The values shown are of cpm of ^{3}H-TTP incorporated in a reverse transcriptase assay measured in cell supernatants sampled at the times indicated post-coculture of 293/2° virus producer cells with each of the cell lines.

Figure 6. A comparison of the deduced amino acid sequences of the *env* genes of PERV-1.15 (SEQ ID NO:3 encoded by SEQ ID NO:18), PERV-A (Letissier et al., 1997; SEQ ID NO:4) and PERV-C (Akiyoshi et al., 1998; SEQ ID NO:5). A schematic representation of the regions of the PERV-1.15 gene homologous to PERV-A (hatched) and PERV-C (open) genes (top figure). The envelope surface (SU) and transmembrane (TM) glycoprotein regions are also shown. Identical amino acids are denoted by a (.); gaps are denoted (_).

Figure 7. Schematic representation of the cloned PERV sequences. A proposed model for a PERV provirus with estimated locations of the viral domains is shown at the top. The PERV sequences contained in the six unique lambda clones are shown compared to the model. The lamA8 *pol* gene contains a 86 nucleotide deletion (del), and the *env* gene contains a 101 nucleotide insertion (ins) compared to all of the comparable sequences.

Figure 8. A comparison of the nucleotide sequences of two PERV LTRs. The LTR sequence of the published cDNA clone PERV-MSL (SEQ ID NO:7) is compared to the lamA1 LTR sequence (SEQ ID NO:6). Identical bases are denoted by (.); gaps are denoted (_). The estimated location of the major regions of the LTR, U3, R, and U5 are indicated. The sequence of the putative tRNA binding site is also indicated (18 of 18 nucleotides identical to the tRNA^{Pro} binding site).

Figure 9. Schematic representation of the construction of recombinant PERV molecular clones.

Figure 10. Analysis of PERV proteins by SDS-PAGE and Western blot. (A) Virus was pelleted by ultracentrifugation through a 20% sucrose pad, separated by 12% SDS-PAGE, and visualized by staining with Coomassie brilliant blue. Lane 1, 5 ml 293 supernatant; lane 2, 5 ml 2°-293/PERV supernatant; lane 3, 15 ml 2°-293/PERV supernatant; lane 4, 5 ml DF-1 supernatant; and lane 5, 5 ml avian leukosis virus infected DF-1 supernatant. (B) Viral proteins were prepared and separated by SDS-PAGE as described above, and transferred to nitrocellulose. Lanes 1, 3, 5 and 7, 5 ml 293 supernatant; and lanes 2, 4, 6 and 8, 5 ml 2°-293/PERV supernatant. Lanes 1 and 2 were exposed to 1:1000 dilution of goat anti-GALV capsid antisera; lanes 3 and 4 to 1:1000 goat preimmune sera; lanes 5 and 6 to 1:1000 goat anti-SSAV capsid antisera; and lanes 7 and 8 to 1:1000 goat preimmune sera. The filters were washed and exposed to peroxidase-labeled rabbit anti-goat antibody. The antibody complexes were detected by chemiluminescence, and exposed to film for 30 seconds. The PERV CA protein migrates at about 25 kDa.

Figure 11. Schematic of sTva antiviral gene constructs and the ALV-based retroviral vectors.

Figure 12. General procedure for using replication-competent ALV-based retroviral vector system *in vitro* and *in vivo*.

Figure 13. sTva-mIgG receptor expression levels in DF-1 cells. The sTva-mIgG protein was immunoprecipitated with goat α-mouse-IgG agarose beads from supernatants (500 µl) of DF-1 cultures infected with the RCASBP(C), RCAS(C) or RCOSBP(C) vectors alone (V) or containing the *stva-mIgG* gene (sTva). The immunoprecipitates were denatured, separated by 12% SDS-PAGE, and analyzed by Western transfer. The filter was probed with peroxidase-conjugated goat anti-mouse IgG, and the bound protein-antibody complexes were visualized by chemiluminescence on Kodak X-Omat film. sTva-mIgG protein expressed transiently in human embryonic kidney 293 cells was included as a positive control (+).

Figure 14. sTva-mIgG expression in sera of chickens infected with RCASBP vectors. The sTva-mIgG protein was immunoprecipitated from chicken serum (500 µl) and analyzed as described (Figure 13 legend). Lane 1, uninfected control; Lane 2, a RCASBP(B) vector alone infected bird; Landes 3-

4, RCASBP(B)stva-mIgG infected birds; Lane 5, a RCASBP(C) vector alone infected bird; Lane 6, a RCASBP(C)stva-mIgG infected bird; Lane 7, RCASBP(C)stva-mIgG infected DF-1 cells as a positive control.

Figure 15. Analysis of viral and soluble receptor RNA levels in tissues of chickens infected with RCASBP(B). The figure shows autoradiograms of 6% polyacrylamide/7.6 M urea gels used to separate the protected RNA probe fragments produced in an RNase protection assay with RNA from a bird infected with RCASBP(B)stva or RCASBP(B)stva-mIgG. RNA was prepared from liver (L), heart (H), spleen (S), bursa (B), thymus (T), kidney (K), and muscle (M) tissues of each bird. RNA from DF-1 cells infected with the appropriate virus was included as a positive control (+). RNA from bursa of an uninfected bird was the negative control (-). ALV(B) *env* RNA protects a 467-nt fragment from the 522-nt ^{32}P-labeled full-length probe [env(B)]; *stva* RNA protects a 388-nt fragment from the 498-nt probe (stva); and *stva-mIgG* RNA protects a 363-nt fragment from the 423-nt probe (stva-mIgG). Each assay contained a chicken GAPDH probe as a control for RNA quality and quantity. GAPDH RNA protects a 200-nt fragment from the 279-nt GAPDH probe.

Figure 16. Analysis of viral and soluble receptor RNA levels in the bursa of birds infected with RCASBP(B) vectors. The figure shows an autoradiogram of a 6% polyacrylamide/7.6 M urea gel used to separate the protected RNA probe fragments produced in an RNase protection assay with RNA from the bursa of birds infected with RCASBP(B) alone (V), RCASBP(B)stva (S), RCASBP(B)stva-mIgG (I), or uninfected (U). RNA from DF-1 cells infected with the appropriate virus was included as a positive control (+). ALV(A) *env* RNA protects a 423-nt fragment from the 483-nt ^{32}P-labeled full-length probe [env(A)]; ALB(B) *env* RNA protects a 467-nt fragment from the 522-nt probe [env(B)]; *stva* RNA protects a 388-nt fragment from the 498-nt probe (stva); and *stva-mIgG* RNA protects a 363-nt fragment from the 423-nt probe (stva-mIgG). Each assay contained a chicken GapDH probe as a control for RNA quality and quantity. GAPDH RNA protects a 200-nt fragment from the 279-nt GAPDH probe. Full-length probes not treated with RNase: lane A, env(A); lane B, env(B); lane S, stva; lane I, stva-mIgG; and Lane G, GAPDH.

Figure 17. Analysis of viral and soluble receptor DNA in tissues of RCASBP(B) infected birds and challenged with RAV-1. Genomic DNA was isolated from liver (L), heart (H), spleen (S), bursa (B), thymus (T), kidney (K), and muscle (M) samples of birds infected with RCASBP(B) alone (I), RCASBP(B)stva (II) and RCASBP(B)stva-mIgG (III) and challenged with RAV-1. DNA isolated from DF-1 cells infected with the appropriate virus was used as a positive control (+). DNA isolated from the bursa of an uninfected control bird was used as the negative control (-). DNA sequences were detected by PCR using specific primer pairs: RAV-1 challenge virus DNA [env(A)] was detected using primers specific for ALV(A) *env* yielding a 937 bp fragment; RCASBP(B) vector DNA [env(B)] was detected using primers specific for ALV(B) *env* yielding a 429 bp fragment; *stva* DNA (stva) and *stva-mIgG* DNA (stva-mIgG) were detected with specific primers yielding fragments of 314 bp and 589 bp respectively. The amplified DNA fragments were separated on 0.8% agarose gels and visualized with ethidium bromide. The molecular weight marker is the 1 Kb plus DNA ladder (Gibco).

Figure 18 A) Nucleotide sequence of env gene of PERV 1.15 (SEQ ID NO:18). B) Nucleotide sequence of PERV sequences in lambda A1 clone (SEQ ID NO:19). C) Nucleotide sequence of PERV sequences in lambda A10 clone (SEQ ID NO:20). D) Nucleotide sequence of PERV sequences in lambda A11 clone (SEQ ID NO:32). E) Nucleotide sequence of PERV sequences in lamba A3A clone (SEQ ID NO:21). F) Nucleotide sequence of PERV sequences in lambda A6 clone (SEQ ID NO:22). G) Nucleotide sequence of PERV sequences in lambda clone A8 (SEQ ID NO:23).

Detailed Description of the Invention

Definitions

As used herein, the terms "isolated and/or purified" refer to *in vitro* preparation, isolation and/or purification of a nucleic acid molecule or polypeptide (e.g., antibody) of the invention, so that it is not associated with *in vivo* substances. Thus, with respect to an "isolated nucleic acid molecule", which includes a polynucleotide of genomic, cDNA, or synthetic origin or some combination thereof, the "isolated nucleic acid molecule" (1) is not associated with all or a portion of a polynucleotide in which the "isolated nucleic acid

molecule" is found in nature, (2) is operably linked to a polynucleotide which it is not linked to in nature, or (3) does not occur in nature as part of a larger sequence. An isolated nucleic acid molecule means a polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide. The term includes single and double stranded forms of DNA. The term "oligonucleotide" referred to herein includes naturally occurring, and modified nucleotides linked together by naturally occurring, and non-naturally occurring oligonucleotide linkages. Oligonucleotides are a polynucleotide subset with 200 bases or fewer in length. Preferably, oligonucleotides are 10 to 60 bases in length and most preferably 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 bases in length. Oligonucleotides are usually single stranded, e.g., for probes; although oligonucleotides may be double stranded, e.g., for use in the construction of a variant. Oligonucleotides of the invention can be either sense or antisense oligonucleotides. The term "naturally occurring nucleotides" referred to herein includes deoxyribonucleotides and ribonucleotides. The term "modified nucleotides" referred to herein includes nucleotides with modified or substituted sugar groups and the like. The term "oligonucleotide linkages" referred to herein includes oligonucleotides linkages such as phosphorothioate, phosphorodithioate, phophoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoraniladate, phosphoroamidate, and the like. An oligonucleotide can include a label for detection, if desired.

The term "isolated polypeptide" means a polypeptide encoded by cDNA or recombinant RNA, or is synthetic origin, or some combination thereof, which isolated polypeptide (1) is not associated with proteins found in nature, (2) is free of other proteins from the same source, e.g., free of human proteins, (3) is expressed by a cell from a different species, or (4) does not occur in nature.

The term "sequence homology" means the proportion of base matches between two nucleic acid sequences or the proportion amino acid matches between two amino acid sequences. When sequence homology is expressed as a percentage, e.g., 50%, the percentage denotes the proportion of matches over the length of a sequence that is compared to some other sequence (the reference sequence). Gaps (in either of the two sequences) are permitted to maximize

matching; gap lengths of 15 bases or less are usually used, 6 bases or less are preferred with 2 bases or less more preferred. When using oligonucleotides as probes or treatments, the sequence homology between the target nucleic acid and the oligonucleotide sequence is generally not less than 17 target base matches out of 20 possible oligonucleotide base pair matches (85%); preferably not less than 9 matches out of 10 possible base pair matches (90%), and more preferably not less than 19 matches out of 20 possible base pair matches (95%).

The term "selectively hybridize" means to detectably and specifically bind. Polynucleotides, oligonucleotides and fragments of the invention selectively hybridize to nucleic acid strands under hybridization and wash conditions that minimize appreciable amounts of detectable binding to nonspecific nucleic acids. High stringency conditions can be used to achieve selective hybridization conditions as known in the art and discussed herein. Generally, the nucleic acid sequence homology between the polynucleotides, oligonucleotides, and fragments of the invention and a nucleic acid sequence of interest is at least 65%, and more typically with preferably increasing homologies of at least about 70%, about 90%, about 95%, about 98%, and 100%. Preferred PERV nucleic acid sequences for use in the methods of the invention are those which have at least about 80%, more preferably 90%, and even more preferably 95%, contiguous nucleotide sequence homology or identity to SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 or SEQ ID NO:32. Preferably, PERV nucleic acid sequences are those which hybridize under moderate, preferably under stringent, hybridization conditions to SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 or SEQ ID NO:32.

Two amino acid sequences are homologous if there is a partial or complete identity between their sequences. For example, 85% homology means that 85% of the amino acids are identical when the two sequences are aligned for maximum matching. Gaps (in either of the two sequences being matched) are allowed in maximizing matching; gap lengths of 5 or less are preferred with 2 or less being more preferred. Alternatively and preferably, two protein sequences (or polypeptide sequences derived from them of at least 30 amino acids in length) are homologous, as this term is used herein, if they have an alignment

score of at more than 5 (in standard deviation units) using the program ALIGN with the mutation data matrix and a gap penalty of 6 or greater. See Dayhoff, M. O., in Atlas of Protein Sequence and Structure, 1972, volume 5, National Biomedical Research Foundation, pp. 101-110, and Supplement 2 to this volume, pp. 1-10. The two sequences or parts thereof are more preferably homologous if their amino acids are greater than or equal to 50% identical when optimally aligned using the ALIGN program.

The term "corresponds to" is used herein to mean that a polynucleotide sequence is homologous (i.e., is identical, not strictly evolutionarily related) to all or a portion of a reference polynucleotide sequence, or that a polypeptide sequence is identical to a reference polypeptide sequence. In contradistinction, the term "complementary to" is used herein to mean that the complementary sequence is homologous to all or a portion of a reference polynucleotide sequence. For illustration, the nucleotide sequence "TATAC" corresponds to a reference sequence "TATAC" and is complementary to a reference sequence "GTATA".

The following terms are used to describe the sequence relationships between two or more polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Generally, a reference sequence is at least 20 nucleotides in length, frequently at least 25 nucleotides in length, and often at least 50 nucleotides in length. Since two polynucleotides may each (1) comprise a sequence (i.e., a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) may further comprise a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity.

A "comparison window", as used herein, refers to a conceptual segment of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2: 482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48: 443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. (U.S.A.) 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by inspection, and the best alignment (i.e., resulting in the highest percentage of homology over the comparison window) generated by the various methods is selected.

The term "sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The terms "substantial identity" as used herein denote a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 85 percent sequence identity, preferably at least 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 nucleotide positions, frequently over a window of at least 20-50 nucleotides,

wherein the percentage of sequence identity is calculated by comparing the reference sequence to the polynucleotide sequence which may include deletions or additions which total 20 percent or less of the reference sequence over the window of comparison.

As applied to polypeptides, the term "substantial identity" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least about 80 percent sequence identity, preferably at least about 90 percent sequence identity, more preferably at least about 95 percent sequence identity, and most preferably at least about 99 percent sequence identity.

Moderate and stringent hybridization conditions are well known to the art, see, for example sections 9.47-9.51 of Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989). For example, stringent conditions are those that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate (SSC); 0.1% sodium lauryl sulfate (SDS) at 50°C, or (2) employ a denaturing agent such as formamide during hybridization, e.g., 50% formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C. Another example is use of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% sodium dodecylsulfate (SDS), and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS.

CTVI

The present invention describes a method of interfering with viral replication. For example, the fusion of an enzyme (such as a nuclease, lipase, or protease) to a viral capsid, glycoprotein or accessory polypeptide which is incorporated into virions can inactivate essential viral components, such as nucleic acid, protein or lipid, which are necessary for replication. This technique is referred to as capsid-targeted viral inactivation (CTVI), although it includes the targeting of non-capsid fusions, e.g., env fusions, to the virion as well.

The present invention uses nucleases, proteases, and/or lipases as antiviral therapeutic agents that degrade or modify essential viral components, such as nucleic acids, proteins, or lipids. The method of the present invention can be applied to viruses that have relatively flexible capsid structures such as retroviruses, lentiviruses, herpesviruses, poxviruses, togaviruses, hepadnaviruses, caulimoviruses, myxoviruses and paramyxoviruses, that readily allow the encapsidation of foreign proteins in an aqueous internal compartment containing the viral nucleic acid. Preferred viruses to be inhibited by the methods of the invention include porcine endogenous retroviruses (PERVs), herpesviruses such as EBV and CMV, and hepatitis viruses, e.g., hepatitis A, B, and C. See Fields, Virology, Lippincourt-Raven, Philadelphia, PA (1996), which is specifically incorporated by reference herein. The enzyme portion of the fusion protein preferably is oriented so that it is internal to the assembled capsid structure. However, externally facing enzymes may be used in the case of proteases and lipases. The use of such constructs does not require the virus to have an aqueous internal compartment. In the case of lipases, it is desirable to target the enzyme to the envelope of the virus. The enzyme portion can be either inside or outside the viral envelope. In this way, any enveloped virus can be targeted by CTVI.

Retroviruses, and the closely related retrotransposons, which are referred to herein generically as retroviruses, are particularly susceptible to CTVI because of their assembly mechanism. It is possible to take advantage of the knowledge of how these capsids assemble to direct a destructive enzyme molecule to the inside surface of the capsid, where it can contract viral nucleic acids or proteins. Retroviral and retrotransposon reverse transcriptases are expressed as natural fusion proteins, in which the polymerase protein forms the C-terminal portion of the primary translation product and the gag protein forms the N-terminal portion. The mechanisms by which Gag-Pol fusion proteins are formed in different retroviruses vary, sometimes involving frameshifting during translation, suppression of a nonsense codon, or splicing. Regardless of the mechanism of synthesis, the reverse transcriptase protein sequence is found at the C-terminus of the Gag protein sequences. In addition, the reverse transcriptase is found internal to the capsid structure. Substitution of a destructive enzyme coding

region for the reverse transcriptase gene (i.e., inserting an open reading frame for a destructive enzyme into the *pol* gene in frame), leads to the assembly of the enzyme in retroviral particles. Further, the nuclease or protease is oriented relative to the capsid in such a way as to have access to the viral RNA or reverse transcriptase. Gag-degradative enzyme fusions, as well as gag-pol-degradative enzyme fusions and env-degradative enzyme fusions, are envisioned. Further, the amino acid linkage between the viral proteins and the degradative enzyme may include sequences that are susceptible to proteases present in the virion, and so are cleaved to yield a soluble degradative enzyme.

Thus, a dominant negative effect is obtained by fusion of a protein with a destructive or modifying enzymatic activity that can alter or destroy an essential component of the virus (e.g., DNA, RNA or protein). The destructive or modifying activity is targeted to the desired site of action (inside or closely adjacent to the virus particle) because it is covalently linked to a core protein of the viral particle, e.g., in the same manner as reverse transcriptase.

Besides its versatility, one of the main advantages of CTVI is that it is enzymatic. It does not rely on massive over-expression of a mutant protein that in some way interferes with the viral life cycle, as is the case in the strategies referenced above. Rather, a small number of enzyme molecules (e.g., nucleases) are incorporated into a viral particle, and they cleave or modify one or more essential components of the virus.

CTVI also has advantages over traditional chemotherapy. Viruses, especially viruses with error-prone replicative mechanisms such as HIV and other retroviruses, are likely to become resistant to a chemotherapeutic agent. For example, HIV isolates resistant to AZT, a widely used anti-HIV drug, have been reported. Clearly, resistance to drugs is an important problem with viral infections just as it is for bacterial infections. Gene therapy or intracellular immunization strategies may also be subject to problems of resistance. For example, if a virus mutates such that the capsid protein no longer assembles with the capsid fusion protein of the present invention, the virus will become resistant to the particular CTVI therapy. However, the DNA of the mutant virus can be cloned and the mutant capsid gene can be fused to the gene encoding a nuclease or other enzyme, thereby restoring the efficacy of the therapy. This approach is

not possible with normal drug therapy; once a virus becomes resistant to a given drug, use of that drug has to be abandoned.

Fusion proteins according to the present invention comprise a destructive enzyme which is capable of destroying the replication ability of a virus or virus-like particle. As used in the present invention, "replication ability" encompasses infectivity of a virus particle or transposition of a retrotransposon. Typically, the destructive enzyme is a nuclease, lipase or protease. Protein-modifying enzymes, such as kinases, which diminish enzyme activity can also be used, for example, one which inactivates a viral encoded polymerase. Fusion proteins also comprise a capsid protein, such as Gag, which confers upon the fusion proteins the ability to co-assemble into a virus particle or envelope protein. As mentioned above, it may be desirable in the case of lipase fusions that the virus-encoded portion of the fusion protein be an envelope protein, rather than a capsid protein.

Nucleases which can be used in the practice of the present invention to make fusions include restriction endonucleases such as EcoRI, and less specific RNAses, such as T1 RNase, barnase, RNase H1, RNase III, retroviral RNase H domains from reverse transcriptase, and staphylococcal nuclease (SN). Other destructive enzymes which can be used in the practice of the present invention include proteases, e.g., nonhomologous retroviral proteases, and lipases. Any such enzymes known in the art can be used. These enzymes degrade proteins and lipids which may be essential for the replication (infectivity) of particular viruses. Other enzymes which modify protein structures may be used, if they result in the inactivation of proteins which are necessary for the viral life cycle. such protein modification enzymes include: kinases, glycosylases, phosphatases, methyl transferases, acetylases, acylases, farnesyl transferases, and demyristylases.

High levels of expression of the fusion proteins are not required, as a single active enzyme molecule can be sufficient to inactivate a virus particle. However, it is desirable that each virus particle formed have at least a single molecule of the fusion protein. Thus, statistical considerations would dictate that expression at a rate greater than one molecule of fusion protein per virus particle be obtained.

In some embodiments of the invention, it may be desirable to utilize conditionally active or marginally active enzymes, since the destructive activity of the enzyme may be deleterious to cells used to prepare the constructs of the present invention. Thus, for example, calcium dependent enzymes may be used, which require a threshold level of calcium for activity. Calcium-dependent destructive enzymes which may be used include calpain, phospholipase A2 and staphylococcal nuclease. It may also be desirable to non-conditionally diminish the activity of the destructive enzyme to a level which is not toxic to cells but which is toxic to viruses. Random mutagenesis can be used to accomplish this end.

DNA molecules are also provided according to the invention, which code for fusion proteins as described above. The DNA molecules comprise appropriate transcriptional and translational control signals which allow the DNA molecules to be expressed in the host cells of the viruses from which the capsid or envelope protein is derived. The expression of the fusion proteins may be dependent upon the presence of virus in the cell.

Recombinant virus is also provided by the present invention. These particles comprise a nucleic acid molecule encoding a fusion protein, as described above. Thus, infection of cells with these recombinant viruses will yield fusion proteins. The recombinant virus is desirably not related to the virus from which the capsid or envelope protein of the fusion protein is derived. The recombinant virus is a mere vehicle for introduction of the fusion constructs. When the cells are infected with viruses which are cognate to the fusion protein capsid or envelope portion, the normal infection cycle of the viruses proceeds. However, when the viruses encapsidate viral nucleic acid, wild-type capsid or envelope proteins co-assemble with fusion proteins. Thus, the newly assembled viruses are hybrids comprising wild-type and fusion capsid or envelope proteins. The newly assembled viruses are not infective because the enzyme portion of the fusion protein inactivates either the viral nucleic acid or the essential viral-packaged proteins or lipid comprising the viral envelope.

Exemplary nucleic acid molecules are those comprising PERV nucleic acid sequences. Thus, for fusion proteins of the invention, it is preferred that nucleic acid molecules encoding PERV capsid or env are employed. For

example, recombinant virus may be obtained from cells, e.g., helper cells, transfected or infected with a recombinant DNA molecule encoding a fusion protein comprising PERV capsid linked to a degradative enzyme. Preferably, once the fusion protein is packaged into virions, the degradative enzyme is proteolytically cleaved from the fusion protein, i.e., it is soluble within the virion.

A method of inhibiting virus replication or infectivity is also provided by the present invention. A nucleic acid molecule encoding a fusion protein is introduced into a cell susceptible to a virus. The fusion protein may comprise a capsid or envelope protein of the virus as well as a destructive enzyme as described above. The method of introducing the nucleic acid molecule into the cell is not critical to the invention, and many such methods are known in the art. These include, without limitation: infection, transformation, transfection, lipofection, tungsten microprojectiles, electroporation, cell fusion, and transduction.

Nucleic acid molecules encoding the fusion protein of the present invention can be introduced into solid organs, tissues or cells, e.g., stem cells of the hematopoietic lineage or B lymphocytes. T-lymphocytes and monocytes/macrophages, which are derived from hematopoietic stem cells, are the primary target of viruses such as HIV. Bone marrow cells can be taken from an individual, and if desired, the stem cells can be purified from the mixed population of marrow cells. The nucleic acid molecules of the present invention can be introduced into the stem cells by means of transfection, or any other means known in the art. The transfected stem cells can then be reinfused into the individual (autologous stem cell transplantation). To facilitate proliferation of the transplanted stem cells, the individual's bone marrow can be partially cleared by irradiation or chemotherapy.

In another embodiment, the nucleic acid molecule of the present invention is introduced into an animal, or gametic cells or embryos. Techniques such as microinjection or transfection can be used, as is well known to the art. The nucleic acid-treated cells can be used in artificial insemination (gametes) or can be reimplanted into a hormone-prepared female animal (embryos) as is known in the art.

In yet another method of introducing the nucleic acids of the present invention into cells or an animal, a recombinant virus can be used. The recombinant virus is desirably derived from a virus having the same cell-type tropism as the virus from which the capsid or envelope protein of the gene fusion is derived. Thus, for example, in order to introduce a gene fusion which employs a PERV capsid protein gene, a PERV viral vector may be used. The recombinant virus is then administered according to a route of viral infection for the particular virus of the vector.

An alternative way for introducing the fusion protein encoding construct of the present invention into cells and animals is by means of hybrid virus particles which contain the nucleic acid of the present invention but do not contain the fusion protein of the invention. Hybrid viruses can be prepared which contain the nucleic acid encoding the fusion protein of the present invention using a packaging cell line. Such cell lines may be propagated in culture according to techniques well known in the art. Such cell lines produce the proteins necessary for packaging viral genomes. The nucleic acids of the present invention can be introduced into such a packaging cell line. Desirably, the nucleic acids will contain the packaging signal which is recognized by the packaging proteins of the cell line. Preferably, the fusion protein gene is under the control of an inducible promoter, such as the metallothionine promoter. When it is desirable to produce viral particles carrying the nucleic acid of the present invention, the inducible promoter can be induced to turn on transcription of the fusion protein gene construct, and a protein synthesis inhibitor, such as cycloheximide, can be added so that the fusion protein transcript is not translated in the packaging cell line. Thus, the fusion protein gene construct is transcribed and packaged into the particles produced by the cell line, without interference from (co-assembly with) the fusion protein. When the packaged particles are used to infect cells, the nucleic acid encoding the fusion protein is expressed, and the fusion protein becomes co-assembled into the progeny particles, rendering them non-infectious.

Methods of producing animals, e.g., humans or other non-human animals, which are resistant to a virus are also provided by the present invention. A nucleic acid molecule which encodes a fusion protein as described above is

introduced into the germ line of an animal or an embryo, or to the animal, e.g., via DNA immunization or by infection with recombinant virus. Methods for the introduction of nucleic acid molecules to animals are known in the art (see, for example, Salter et al., 1991; Salter et al., 1989; Heninginghausen, 1990; Ebert et al., 1991; Wright et al., 1991; Jaenish, 1988; Wagner et al. (U.S. Patent No. 4,873,191); Donahue et al., 1992; Rogers et al., 1993). All somatic cells resulting from development of zygotes containing the nucleic acid molecule are resistant to the virus from which the fusion protein capsid or envelope portion is derived. Methods for making transgenic animals which carry foreign genes in each cell of the animal are known in the art.

Receptor Interference (RI)

Another antiviral strategy targets the first step in the virus life cycle, the interaction of the viral envelope glycoprotein(s) with a host cell receptor. For example, retroviral infection of cells can be significantly reduced by expressing soluble forms of the host receptor, which bind the glycoproteins of the incoming virions before the virion can bind to the host receptor, or the viral envelope glycoproteins (the product of the *env* gene), which block the host receptors, directly preventing virion binding.

There are at least two distinguishable steps in viral entry; the first involves recognition and binding of the viral envelope glycoprotein to the host receptor, the second involves steps that lead to the fusion of the host and viral membranes. The *env* gene of retroviruses and lentiviruses encodes a polyprotein precursor that is subsequently processed into two glycoproteins, the surface glycoprotein (SU) which contains the domains that interact with the host receptor, and the transmembrane glycoprotein (TM) that anchors the SU protein to the membrane and appears to be directly involved with the fusion between the virus and cell membranes. Following membrane fusion, the viral core is released into the cytoplasm where the single-stranded RNA genome found in the virion is copied into double-stranded DNA (dsDNA) by the viral enzyme reverse transcriptase (RT). This reverse transcription process produces a linear dsDNA that is longer than the RNA genome from which it derives. The ends of the linear DNA contain terminally redundant sequences known as long terminal repeats (LTRs). Retroviruses, and vectors that derive from them, appear to

require the breakdown of the nuclear membrane that occurs during mitosis for the viral DNA to gain access to the cellular genome. Once this occurs, the linear viral DNA is inserted into the host genome by the virally encoded enzyme integrase (IN). The integrated viral DNA is called a provirus. Efficient production of progeny viruses requires the integration of the viral genome into host DNA.

Cells and animals engineered to express envelope glycoproteins have been shown to be highly resistant to that strain of retrovirus and to have less virus-associated pathogenesis (Federspiel et al., 1989; Nihrane et al., 1996; Salter et al., 1989). Based on the receptor interference of endogenous ALV(E), Salter and Crittenden (1989) proposed that insertion of the ALV(A) envelope gene into the germline of chickens and its subsequent expression would provide resistance to infection by ALV(A). Their initial germline studies produced 23 lines of transgenic chickens using ALV-based retroviral vectors and proved two major points. First, these studies showed that avian retroviruses can be artificially inserted into the germline of chickens at a reasonable efficiency, stably inherited by subsequent generations, and that the viral genes were expressed (Crittenden et al., 1989; Salter et al., 1987). Second, these studies showed that expression of the inserted subgroup (A) envelope glycoproteins could inhibit subsequent ALV(A) infection by subgroup-specific receptor interference, both *in vitro* and *in vivo* (Salter et al., 1989; Salter et al., 1991).

Two transgenic chicken lines, *alv6* and *alv11*, that did not produce infectious virus were extensively characterized at the RNA level in different tissues and at different stags of development. Viral RNA was expressed by both lines in all tissues tested regardless of the stage of development; insert *alv6* expressed moderate levels of *env* RNA, while insert *alv11* expressed low levels of *gag* and *env*. Both lines, however, expressed much higher levels of viral RNA in the tissues associated with ALV pathogenesis, the bursa, thymus, and spleen. *In vitro*, both *alv6* (about 4400-fold) and *alv11* (about 11-fold) chicken embryo fibroblasts (CEF) were resistant to ALV(A) infection. The susceptibilities of the *alv6* and *alv11* transgenic lines to ALV(A) infection and associated pathogenesis were compared to other properties (e.g., resistance measured *in vitro, env* expression levels, etc.) to determine which characteristics were important

indicators of an antiviral effect *in vivo*. None of the *alv6* birds were productively infected as determined by the absence of both infectious ALV(A) and ALV(A) neutralizing antibodies, while two-thirds of the *alv11* birds were productively infected by ALV(A). However, neither the *alv6* nor the *alv11* chickens showed significant ALV-induced pathogenesis. Thus, the level of Env glycoprotein expressed in the target tissues for ALV pathogenesis determined the magnitude of ALV interference (Federspiel et al., 1991).

Reticuloendotheliosis virus (REV) is very cytotoxic to avian cells *in vitro* presumably due to the fusionogenic properties of the envelope glycoproteins, especially the TM glycoprotein. REV stocks are therefore produced in D17 cells, a canine osteosarcoma line tolerant to REV infection. D17 cell lines expressing the REV envelope glycoproteins were significantly more resistant to REV infection (up to 25,000-fold) compared to controls. However, when the same REV envelope expression cassette was delivered into chicken embryo fibroblasts (CEF), the REV envelope gene sustained large deletions and the envelope proteins were not expressed due to cytotoxicity of the REV envelope glycoproteins to CEF cells. Thus, to reduce potential cytotoxic effects, it is preferred that soluble forms of viral envelope glycoprotein are employed. The soluble protein differs from the wild-type protein in that it lacks the transmembrane (TM) domain which anchors the protein in the membrane, and are therefore secreted from the cell.

The invention will be further described by the following examples.

Example 1

Expression of a Mo-MLV Gag-*E. coli* RNase H Fusion Polyprotein

A gene encoding a Mo-MLV Gag-*E. coli* RNase HI fusion was constructed by linking the RNase HI coding region to the Mo-MLV Gag polyprotein six codons upstream of the Gag termination codon (Van Brocklin et al., 1997). The RNase HI coding sequence was isolated from *E. coli* DNA by PCR amplification with a 5′ primer containing a BglII site (5′-GCG CAT GCA GAT CTG ATG CTT AAA CAG GTA GAA ATT TTC ACC GAT GG-3′; SEQ ID NO:1) and a 3′ primer containing a SalI site (5′-GCT GCT GCG TCG ACT TAA ACT TCA ACT TGG TAG CCT GTA TCT TCC-3′; SEQ ID NO:2). The reagents and conditions used for the PCR were as described in Federspiel et al.

(1996). The *E. coli* RNase HI fragment was sequenced and contained one silent nucleotide difference from the sequence published by Kanaya and Crouch (1983), at nucleotide 470 (A→G). The Mo-MLV Gag-RNase H fusion construct was based on the design of the Mo-MLV Gag-SN fusion which has been used to introduce SN into virions (Natsoulis et al., 1995).

The genes encoding the CTVI constructs were delivered into CEF by the RCASBP(A) retroviral vector and expressed under the control of the viral promoter-enhancer in the long terminal repeat. CEF were cultured and passaged every 2 days when they reached confluence (Federspiel et al., 1994). ALV retroviral vector propagation was initiated by transfection of plasmid DNA that contained the retroviral vector in a proviral form by the calcium phosphate precipitation method (Kingston et al., 1989). The course of the retroviral infection was monitored by assaying culture supernatants from confluent cells for the viral Gag protein. Three plasmids were used for comparison: Mo-MLV Gag-SN plasmid pGN1600 (Natsoulis et al., 1995); Mo-MLV Gag plasmid pGN1601 (Natsoulis et al., 1995), which produces only the Mo-MLV Gag polyprotein; and Mo-MLV Gag-SN* plasmid pGS293 (Schumann et al., 1996), which differs from Mo-MLV Gag-SN in two missense mutations in the SN gene that result in an inactive SN enzyme. Maximum levels of Mo-MLV Gag, Mo-MLV Gag-RNase H, Mo-MLV Gag-SN, and Mo-MLV Gag-SN* were seen 10 to 14 days posttransfection, which coincided with maximum RCASBP(A) production. Immunoblot analysis indicated that the Mo-MLV Gag-RNase H polyprotein was expressed at a lower level than Mo-MLV Gag or Mo-MLV Gag-SN. Several viral proteins that were smaller than the expected full-length polyproteins were also observed. These proteins were the likely result of partial degradation of the Pr85 or Pr65 polyprotein associated with the virion isolation procedure, since smaller Gag-associated proteins were also seen in the Mo-MLV Gag control. Southern blot analysis of genomic DNA isolated from day 24 cultures detected only intact proviruses. An *in situ* RNase H assay showed that virus particles isolated from CEF expressing the Mo-MLV Gag-RNase H polyprotein contained high levels of RNase H activity. Little or no RNase H activity was detected in any other culture supernatants.

~~CEF Expressing the Mo-MLV Gag-RNase H Polyprotein Significantly~~ Inhibit Mo-MLV Spread. The antiviral effect of the CTVI fusions expressed by the CEF cultures was measured first in a prophylaxis assay. The cultures were challenged with a low dose (multiplicity of infection [MOI] of 0.05 to 0.1 focus-forming units [FFU] per cell) of amphotropic Mo-MLV strain Mo(4070A) (Ott et al., 1990; Ott et al., 1992). Mo(4070A) is an engineered hybrid Mo-MLV that contains the *env* gene and a portion of the *pol* gene of the amphotropic 4070A virus. The Mo(4070A) virus stock was produced on NIH 3T3 cells (1×10^6 to 2×10^6 FFU/ml). Infectious virus was quantitated by the S+L− focus assay on D56 cells (Bassin et al., 1971). The CEF cultures, which were dividing rapidly, were passaged for 14 days after Mo(4070A) infection. Infectious Mo(4070A) was quantitated at day 14 by the S+L− focus assay (Table 1). CEF expressing the Mo-MLV Gag-RNase H polyprotein reduced the level of infectious Mo(4070A) produced by more than 1,500-fold compared to the Mo(4070A)-infected CEF control.

Table 1. Inhibition of Mo-MLV spread by CTVI[a]

Construct used for treatment	Titer (FFU/ml)[b] (fold inhibition)[c] Expt 1	Expt 2
None (mock treatment)	1.6×10^5	2.1×10^5
Vector alone	2.4×10^4 (6.6)	ND[d]
Mo-MLV Gag	2.5×10^4 (6.3)	4×10^4 (5)
Mo-MLV Gag-RNase H	1×10^2 (1,550)	9×10^1 (2,330)
Mo-MLV Gag-SN	5×10^1 (3,100)	1.6×10^1 (13,125)
Mo-MLV Gag-SN*	1.9×10^4 (8.4)	ND

[a] In a prophylaxis assay, CEF cultures seven passages after transfection with plasmids containing the RCASBP(A) retroviral vector-CTVI constructs were challenged with Mo(4070A) (multiplicity of infection, 0.05 to 0.1 FFU per cell). Infectious Mo(4070A) levels were quantitated from supernatants 14 days postinfection by S+L− focus assays. This experiment was performed twice.

[b] Titers were averages of duplicate assays.

[c] Fold inhibition was determined by comparing the Mo(4070A) titers of the experimental constructs to the Mo(4070A) titer on mock-treated CEF.

[d] ND, not done.

Several cultures were further characterized over the course of the 14-day Mo(4070A) infection by quantitating the levels of infectious Mo(4070A) by S+L- focus assay and analyzing the expression levels of the Mo-MLV Gag and RCASBP(A) Gag polyproteins by Western immunoblotting. The amount of infectious Mo(4070A) produced peaked 7 to 8 days after infection in the control cultures (CEF alone and CEF expressing Mo-MLV Gag), and the titer remained relatively constant over the next 6 days. In contrast, the amount of infectious Mo(4070A) produced by CEF expressing either the Mo-MLV Gag-RNase H or Mo-MLV Gag-SN polyprotein was significantly inhibited, although the levels of infectious virus slowly increased over the course of the experiment. Mo(4070A) virus production was also monitored by the appearance of the Mo-MLV CA protein (about 30 kDa) on immunoblots. The levels of expression of the Mo-MLV Gag, Mo-MLV Gag-RNase H, and Mo-MLV Gag-SN polyproteins remained relatively constant throughout the experiment. At late time points post-Mo(4070A) infection (days 12 to 14), the Mo-MLV Gag polyprotein levels may decrease slightly due to proteolytic processing by protease from the infectious Mo(4070A). The levels of the MA protein (about 19 kDa) from the RCASBP(A) retroviral vector remained relatively constant throughout the experiment.

The Mo-MLV Gag-SN fusion polyprotein was tested in parallel with the Mo-MLV Gag-RNase H fusion to provide a direct comparison to a characterized CTVI construct known to have antiviral activity. Unexpectedly, the antiviral effect of Mo-MLV Gag-SN was 100-fold greater in the experiments reported herein (> 3,000-fold [Table 1]) than that previously observed (about 30-fold [Natsoulis et al., 1995]). The increase in the antiviral effect may be due to an increase in the efficiency of producing CEF cultures that express higher levels of the fusion polyprotein. The CEF themselves grew at a faster rate, presumably due to changes in the growth media including different serum lots. This difference in growth rate was especially apparent in CEF infected with Mo(4070A). In previous experiments, Mo(4070A) infection dramatically slowed the growth of CEF and caused some cytotoxicity.

In the experiments reported herein, all CEF cultures grew at the same rate until natural senescence. A consistent six- to eight-fold inhibition of Mo(4070A)

titer was observed in cells expressing the control constructs, including cultures that expressed RCASBP(A) vector (Table 1), that was not detected previously (Natsoulis et al., 1995; Schuman et al., 1996). Although this may be related to the "steric effect" (three- to five-fold) of the Mo-MLV Gag-SN* polyprotein on Mo(4070A) virus production observed by Schumann et al. (1996), the decrease in the Mo(4070A) titers produced in cultures that expressed RCASBP(A) suggests that the RCASBP vector may alter cells in ways that interfere with Mo-MLV virus production, leading to a slight overestimate of the CTVI effect. While several CTVI constructs have significant antiviral effects when used prophylactically, the levels of infectious virus do increase during the experiment. The production of a small number of viruses that do not contain CTVI-derived polyproteins most likely accounts for the small number of infectious viruses needed to spread the infection. Mutations in the *gag* gene capable of circumventing this antiviral strategy would likely be exceedingly rare since they would require the selection of Gag mutants that would still assemble normally but be able to exclude Gag-degradative enzyme polyproteins from virions.

Delivery of the Mo-MLV Gag-RNase HI Fusion Polyprotein to Mo-MLV-Infected CEF has a Therapeutic Effect. To assess the therapeutic potential of the CTVI strategy, CEF chronically infected with Mo(4070A) were transfected with the RCASBP(A) retroviral vector plasmids containing the Mo-MLV Gag fusions and passaged for 16 days. For the therapy assay, CEF chronically infected with Mo-MLV were generated by infecting 4×10^6 cells with 2×10^6 FFU of Mo(4070A) (1 ml of virus stock) and passaging the culture four to six times to allow maximum spread of the virus. The Mo(4070A)-infected CEF cultures produced a maximum titer of 3×10^5 to 4×10^5 FFU/ml as quantitated by the S+L− focus assay. The RCASBP virus spread through Mo(4070A)-infected CEFs with kinetics similar to the spread on CEF that had not been infected with Mo(4070A), reaching maximum levels after about 8 days as determined by Western analysis of ALV MA levels. The levels of infectious Mo(4070A) were quantitated throughout the experiment. The Mo(4070A) titers at 14 days posttransfection in two experiments are shown in Table 2. The level of infectious Mo(4070A) was reduced 7.5- to 18-fold in CEF expressing the Mo-MLV Gag-RNase H polyprotein and 15- to 38-fold in CEF expressing the Mo-

MLV Gag-SN polyprotein. Infection with the RCASBP(A) vector alone or RCASBP(A) expressing the Mo-MLV Gag polyprotein lowered the titer of Mo(4070A) produced by a chronically infected culture two- to three-fold compared to Mo-MLV-infected CEF. This suggests that only a slight therapeutic effect is directly attributable to the CTVI constructs once the infection is established.

Table 2. Inhibition of Infectious Mo-MLV Produced after CTVI Treatment[a]

	Titer (FFU/ml)[b] (fold inhibition)[c]	
Construct used for treatment	Expt 1	Expt 2
None (mock treatment)	3×10^5	3.8×10^5
Vector alone	1.5×10^5 (2)	ND[d]
Mo-MLV Gag	1×10^5 (3)	1.6×10^5 (2.4)
Mo-MLV Gag-RNase H	4×10^4 (7.5)	2.1×10^4 (18)
Mo-MLV Gag-SN	2×10^4 (15)	1.3×10^4 (29)

[a] In a therapy assay, CEF chronically infected with Mo(4070A) were transfected with plasmids containing the RCASBP(A) retroviral vector-CTVI constructs. Levels of infectious Mo-MLV in supernatants were quantitated 14 days posttransfection by S+L− focus assays. The experiment was performed twice.

[b] Titers were averages of duplicate assays.

[c] Fold inhibition was determined by comparing the mo-MLV tiers of the experimental constructs to the Mo-MLV titer on mock-treated CEF.

[d] ND, not done.

Cleavage of the Mo-MLV Gag-Nuclease Fusion Junction by the Incoming Mo-MLV Protease. An Mo-MLV Gag polyprotein fusion junction was designed that could be cleaved by the protease of an incoming infectious Mo-MLV by including the region six amino acids on either side of the normal Mo-MLV protease cleavage site (PRCS). The new Gag fusion plasmid moves the BamHI site to a position just downstream of the Gag termination codon (pMGagPRCS). The termination codon was changed to a codon for glutamine, the same amino acid that Mo-MLV inserts during suppression of the stop codon when the Gag-Pol polyprotein is produced. Genes encoding the Mo-MLV Gag PRCS-RNase H and Mo-MLV Gag PRCS-SN polyproteins were prepared to determine if cleavage of the RNase HI or SN domain from the polyprotein would

increase the antiviral effect. A prophylaxis assay was used to measure Mo(4070A) production in cells expressing the Mo-MLV Gag PRCS fusions and the original Mo-MLV Gag fusions. Addition of the PRCS did not alter the level of inhibition by the RNase HI or SN polyprotein, nor did inclusion of the PRCS alter the therapeutic antiviral effect of either the Mo-MLV Gag-RNase H or the SN polyprotein. Virion proteins isolated from day 16 of the therapy assay of Mo-MLV-infected CEF and CEF expressing Mo-MLV Gag, Mo-MLV Gag-RNase H, and Mo-MLV Gag PRCS-RNase H were assayed for RNase H activity by *in situ* RNase H assay. Only virions from Mo-MLV Gag-RNase H and Mo-MLV Gag PRCS-RNase H cultures contained measurable RNase H activity. A new protein with RNase H activity about 22 kDa was observed in virions obtained from cultures expressing the Mo-MLV Gag PRCS-RNase H polyprotein. Presumably, this protein, which corresponds in size to *E. coli* RNase HI, is the RNase HI domain cleaved from the Mo-MLV Gag PRCS-RNase H polyprotein by the Mo-MLV protease. The ability to release a degradative enzyme from the polyprotein should make it possible to design

future CTVI fusions in which activation of the degradative enzyme is controlled by protease cleavage (e.g., a zymogen), which would allow the use of degradative enzymes whose expression would otherwise be too toxic for the cell.

CTVI Inhibition of Mo-MLV Replication in Avian DF-1 Cells. Line 0 CEF have been the cells of choice for the study of ALV, since line 0 does not contain endogenous loci related to ALV and produces high ALV titers. However, CEF are primary cells and have a limited life span (i.e., about 25 passages). Recently, a permanent cell line was derived from line 0 CEF, named DF-1 (Dr. Douglas Foster, University of Minnesota). Previously, permanent avian cell lines have been unsatisfactory for many ALV studies due to the poor growth of ALV or the presence of interfering exogenous and/or endogenous viruses. The growth of ALV-based retroviral vectors and Mo-MLV was compared in DF-1 and CEF. The DF-1 and CEF cells grow at similar rates and support vigorous growth of ALV and Mo-MLV. The rate at which both ALV and Mo-MLV reach maximum titers, and the level of viral protein produced, is approximately the same in either cell type. The titer of the ALV-based retroviral vectors is 5-10-fold higher when produced in DF-1 cells compared to CEF. A slight increase in the titer of Mo(4070A) viral stocks was obtained when grown in DF-1 cells compared to CEF. These data demonstrate that the DF-1 permanent cell line can be used to test antiviral strategies *in vitro*, and also to generate clonal cell lines that support vigorous ALV replication. Table 3 summarizes the CTVI antiviral effects on Mo-MLV replication in DF-1 cells both prophylaxis and therapy assays.

In animal model systems, it is possible to deliver genes by using either DNA microinjection or retroviral infection into an embryo. This eliminates the host's immune response, and such methods can be used to deliver genes efficiently. Thus, the CTVI strategy may be useful *in vivo*, e.g., in animal systems in which viral infections have important economic consequences (e.g., agriculture), or in non-human transplant tissues.

Table 3. CTVI inhibition of Mo-MLV replication in avian DF-1 cells

Construct	Titer (FFU/ml)[a](fold inhibition)[b]		
	Prophylaxis Assay[c]	Therapy Assay[d]	
		1st Delivery[e]	2nd Delivery[f]
None (mock)	3×10^5	2×10^5	2.1×10^5
Mo-MLV Gag	1.2×10^5 (2.5)	1.4×10^5 (1.4)	1.4×10^5 (1.5)
Mo-MLV Gag-RH	<10 (>30,000)	1×10^2 (2,000)	<10 (>21,000)
Mo-MLV Gag-SN	<10 (>30,000)	1×10^2 (2,000)	<10 (>21,000)

[a] Titers were averages of duplicate assays.
[b] Fold inhibition was determined by comparing the Mo(4070A) titers of the construct to mock-treated DF-1 cells.
[c] DF-1 cells chronically infected with RCASBP(A)-CTVI construct were challenged with Mo(4070A) (multiplicity of infection, 0.05-0.1 FFU per cell). Infectious Mo(4070A) levels were quantitated from supernatants by S+L- assay 30 days post-infection.
[d] DF-1 cells chronically infected with Mo(4070A) were infected with RACSBP(A)-CTVI or RCASBP(C)-CTVI construct viruses. The levels of infectious Mo(4070A) in supernatants were quantitated by S+L- assay 30 days post-infection.
[e] RCASBP(A)-CTVI viruses were used to initiate the therapy assay with the maximum antiviral effect achieved at 30 days.
[f] The antiviral constructs were delivered a second time by the RCASBP(C) vectors.

Example 2

Human Tropic PERVs Produced by Pig Primary PBMC

Methods

Cells and Cell Culture. The cell lines used were either obtained from the ATCC unless otherwise indicated. 293 human embryonic kidney (ATCC CRL-1573), MMK *Mus musculus molossinus* kidney (ATCC CRL-6439), SC-1 mouse embryo epithelial cells (ATCC CRL-6450), ST-IOWA (pig fetal testis), 1o PT (pig testis), MDTF *Mus dunni* tail fibroblast (kindly provided by Olivier Danos), NRK normal rat kidney cells (ATCC CRL-6509), Rat2 rat embryo fibroblasts (ATCC CRL-1764), SIRC rabbit corneal fibroblast (ATCC CCL-60), D17

canine osteosarcoma (ATCC CRL-6248), MDBK bovine kidney epithelium (ATCC CCL-22), FRHK4 rhesus monkey kidney cells (ATCC CRL-1688), Mv1Lu mink lung epithelial cells (ATCC CCL-64), MiCL.1 (S+L-) mink lung (ATCC CCL-64.1), Fc3TG feline tongue fibroblast (ATCC CCL 176), AK-D feline lung epithelial cells (ATCC CCL-150), CRFK feline kidney epithelial cells (ATCC CCL-94), CaKi-1 clear cell kidney carcinoma (ATCC HTB-46), HeLa cervical adenocarcinoma (ATCC CCL-2), HOS human osteosarcoma (ATCC CRL-1543), CaCo-2 colorectal adenocarcinoma (ATCC HTB-37) were maintained in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum (FBS), 2 mM glutamine, 1 mM sodium pyruvate, 100 U of penicillin per m1, and 100 µg of streptomycin per ml. PG-4 feline glial and astrocytes (ATCC CRL 2032) were maintained in McCoy's 5A medium supplemented with 15% FBS, 2 mM glutamine, 1 mM sodium pyruvate, 100 U of penicillin per ml, and 100 µg of streptomycin per ml. HepG-2 hepatoblastoma (ATCC HB-8065) and HT1080 fibrosarcoma (ATCC CCL-121) were maintained in Eagle's Modified Essential Medium supplemented in a similar manner. The following cell lines were maintained in RPMI 1640 supplemented with 10% FBS, 2 mM glutamine, 0.05 mg gentamicin sulfate per ml, 1X non-essential amino acids (Biofluids, Rockville, MD): Molt 4 acute lymphoblastic (ATCC CRL-1582), Daudi Burkitt's lymphoma (ATCC CCL-213), Raji Burkitts lymphoma (ATCC CCL-86), U937 histiocytic lymphoma (ATCC CRL 1593.2) UCLA-SO-M14 T cells (Ramsdell et al., 1988), and the human natural killer cell line YTN10 (Yodoi et al., 1985). PBMCs were obtained from NIH and Yucatan minipigs.

Primary pig aortic endothelial cells are isolated by incubating the inner layer of pig aortas with 0.2% collagenase type I for 20 minutes at 37°C. Detached cells are washed with phosphate-buffered saline, and cultured in M199 medium supplemented with 10% fetal bovine serum, 25 mM HEPES, 2 mM glutamine, 100 U per ml of penicillin, and 100 µg streptomycin. Cultures are fed three times per week and subpassaged every 4-7 days.

Pig hepatocytes are isolated by a two-step perfusion technique as described by Sielaff et al. (1995). The liver is treated by systemic heparinization before isolation. The liver is then treated with an EDTA and collagenase D

solution to free the hepatocytes. The hepatocytes are isolated by gently combing the liver, washing the dislodged cells in Williams E medium supplemented with 5% calf serum, 2 mM L-glutamine, 15 mM HEPES, 1.5 mg/ml insulin, 100 U penicillin per ml and 100 µg streptomycin per ml. The freshly harvested hepatocytes are cultured in collagen gel.

Derivation of viral pseudotypes. Cells productively infected with wild-type PERV were superinfected with retroviral vector-containing supernatant harvested form PA317/G1BgSvN (McLaughlin et al., 1993), in a manner similar to that previously described (Leverett et al., 1998), to generate PERV pseudotypes carrying the murine retrovirus genome coated by PERV core and envelope proteins. G1BgSvN-containing cells were selected in 187 µg/ml G418 (active component). After 10-14 days selection, G418-resistant colonies were pooled and used to generate viral pseudotypes. Since the G1BgSvN vector genome contains the coding sequence for both neomycin phosphotransferase and for β-galactosidase, pseudotype infection is monitored by the acquisition of target cell resistance to G418 or by immunohistochemical detection of target cells expressing β-galactosidase.

Infectivity assays. Supernatant infections were used to determine the infectivity of cell-free virus derived from different producer cell lines. Comparisons between fresh and frozen virus-containing supernatants demonstrated that storage of viral supernatants at -70°C resulted in > 100-fold decrease in infectious titer. Therefore, all experiments are performed using freshly harvested supernatant. On the day prior to initiating an infectivity assay, target cells were seeded at 3-5 x 10^4 cells per well in 12-well dishes. On the next day, supernatant from post-confluent cultures of virus producer cells was harvested, filtered through a 0.45 µm filter, adjusted to 6 µg/ml polybrene and used to replace the medium on target cells. On the following day, the cells were fed with fresh medium. When β-galactosidase expression was used to monitor infectivity, the cells were fixed and histochemically stained 48-72 hours post-exposure to viral supernatant and observed microscopically to enumerate blue-staining foci of cells (BFU/ml), as described elsewhere (Wilson et al., 1991). If the experiment was performed to assess productive infection of the target cell,

the cells would be passaged 1-2 times per week as needed during the course of the experiment and monitored as described below.

The coculture of target cells with virus-producer cells was used to assess the ability of the virus to be transmitted to non-adherent cells. Since several different cell types were used as a source of virus-producer cells in these experiments, the dosage of irradiation required to ensure the virus-producer cells would die within 5 days after irradiation was first determined. Three to four x 10^6 cells for each virus-producer cell line were subjected to 2,000,5,000 or 10,000 rads (using a ^{137}Cs source, Nordion GammaCell 100) and seeded into a 96-well plate at 2-3 x 10^5 cells/well. Irradiated and control non-irradiated cells were monitored for proliferation daily for 5 days by measuring [^{3}H]TTP uptake after cells were cultured for 8 h with 1.0 μCi [^{3}H]TTP (6.7 Ci/mmol; Dupont NEN, Boston, MA), harvested (Skatron, Sterling, VA) and processed for scintillation counting. Based on these findings, the following conditions were used: Daudi cells received 2000 rad, Molt4 and U937 received 5000 rads.

When the target cells in the coculture were human peripheral blood mononuclear cells (hPBMC), the mononuclear layer was collected from a buffy coat from a human donor separated by lymphocyte separation medium (Organon Teknika, Durham, NC). Cells were stimulated in 1X PHA (according to manufacturer's instructions, Life Technologies, Gaithersburg, MD) for 3 days and then mixed in a 1:1 ratio with 3 x 10^6 lethally irradiated virus-producer cells in 12-well dishes. Thereafter, the cocultures were maintained in RPMI 1640 medium supplemented with 10% FBS, 10% purified human IL-2 (Boerhinger Manheim), 10 ng/ml recombinant human IL-2 (Chiron Corporation, Emeryville, CA) 2 mM glutamine, 100 U penicillin, and 100 μg per ml of streptomycin. Control wells containing irradiated virus-producer cells only were monitored for cell viability by visualizing samples microscopically for trypan blue exclusion. Cocultures containing 293 cells as target cells were carried out in parallel as a control for the infectivity of the virus-producer cells. After initiation of the coculture, the next day the medium was replaced with fresh medium and cells were sub-cultured 1-2 times/week as needed. Cocultures containing the hPBMC as targets were reinfused every two weeks with freshly-stimulated hPBMC from the same buffy coat of cells. Methods to monitor virus infection of target cells.

Infection of target cells was assessed by one of three different methods. In some cases, the titer of infectious virus pseudotypes was determined by β-galactosidase expression. Cells were histochemically stained 48-72 hours after exposure to virus-containing supernatant, and foci of β-galactosidase expressing blue cells were counted (BFU/ml). Those titers were then normalized to the titer observed on 293 cells exposed to the same viral supernatant and are reported as % of control. The titer observed on 293 cells ranged 10-fold from several hundred BFU/ml to 2-3,000 BFU/ml.

Virion isolation and purification. Culture supernatants are harvested from infected cells, cleared of floating cells and debris by centrifugation at 3000 × *g* for 10 minutes, and the virus stocks stored at -80°C. Virions are isolated for RT assays and Western analysis by ultracentrifugation of 10 ml virus stock underlaid with 1 ml 20% sucrose at 35,000 rpm in a Beckman SW40 rotor for 1 hour at 4°C to pellet the virus (Federspiel et al., 1994). The viral pellet is then resuspended in either RT assay buffer or Laemmli load buffer.

PERV virions are further purified for antibody production either by sucrose equilibrium density centrifugation or by a sucrose step gradient to concentrate the virions and remove proteins, nucleic acids and ribosomes from the cell supernatants. For equilibrium gradients, the supernatants are mixed with sucrose to a density slightly higher than 1.16 g/ml, the average buoyant density of retroviral particles, and the gradient formed by ultracentrifugation. Viral supernatants are layered onto a two-step sucrose gradient, 20% and 50%, and the virions banded at the boundary between the sucrose steps. In both methods, the banded virions are harvested by removing the band with a syringe through the side of the tube to prevent contamination.

PCR. Standard PCR reactions contains 1.25 µl of 10X PCR buffer (50 mM Tris, pH 8.3, 50 mM KCl, 7 mM $MgCl_2$), 1.25 µl of 1.7 mg/ml BSA, 0.5 µl of each dNTP at 25 mM, 0.56 µl of each oligonucleotide primer (A_{260} = 5), 0-8% dimethyl sulfoxide, 4.2 µl water, and 1 µl genomic DNA (about 100 µg/ml) (Federspiel et al., 1996). The reactions are heated to 90°C and initiated with 1.5 µl *Taq* DNA polymerase (0.75 units). Thirty cycles of PCR are carried out as follows: 90°C for 20 seconds, then 59°C for 80 seconds. Alternations of this basic protocol follow the recommendations of the polymerase manufacturer.

Three sets of primers specifically amplify the three PERV envelope subgroups in the SU glycoprotein region: (all primers listed 5′-3′) PERV-A: TGGAAAGATTGGCAACAGCG and AGTGATGTTAGGCTCAGTGG (SEQ ID NO:8 and SEQ ID NO:9, respectively); PERV-B: TTCTCCTTTGTCAATTCCGG and TACTTTATCGGGTCCCACTG (SEQ ID NO:10 and SEQ ID NO:11, respectively); PERV-C: CTGACCTGGATTAGAACTGG and ATGTTAGAGGATGGTCCTGG (SEQ ID NO:12 and SEQ ID NO:13, respectively). PCR products were separated on a 1.0% agarose gel and DNA fragments of 2-2.5 kB were purified using Qiaex gel purification kit (Qiagen, Valencia, CA). Purified PCR products were then cloned into the TA vector using the TA Cloning Kit (In Vitrogen, Carlsbad, CA). Restriction analysis of clones derived from the TA vector was used to ensure an insert of the appropriate size was present. A minimum of 4 representative clones was chosen for sequence analysis. All deoxynucleotide sequencing was performed by the Mayo Clinic Molecular Biology Core on a Perkin Elmer ABIPRISM™ 377 DNA Sequencer (with XL Upgrade) with the PE applied Biosystems ABI PRISM™ dRhodamine Terminator Cycle Sequencing Ready Reaction Kit with AmpliTaq DNA Polymerase (PE Applied Biosystems, Foster City, CA). The ClustalW Multiple Sequence alignment Program of Mac Vector 6.0.1 (Oxford molecular Group) was used to compare the deduced envelope amino acid sequences.

Sub B1 > RT-PCR. RNA is isolated from virions with RNA STAT 50-LS or STAT-60 (Tel-Test, Inc., Friendswood, TX), and converted to cDNA with 2.5 μM random hexanucleotide primers and Superscript II (Life Technologies, Gaithersburg, MD) (Wilson et al., 1998). cDNA templates are amplified with primers corresponding to the PERV *pol/env* gene boundary (ACCTCGAGACTCGGTGGAAGGG; SEQ ID NO:14) and the untranslated region 3′ of the PERV *env* gene (CTGGGTTCTGGGAGGGTTAGGTTG; SEQ ID NO:15), or amplified with PB906 (5' ACGTACTGGAGGAGGGTCACCTGA 3'; SEQ ID NO:16) and PB908 ('5 GTCCCGAACCCTTATAACCTCTTG 3'; SEQ ID NO:17) or PERVenv1 (sense) (5' ACCTCGAGACTCGGTGGAG; SEQ ID NO:11) and PERVenv2 (anti-sense) (5' CTGGGTTCTGGGAGGGTTAGGTTG; SEQ ID NO:12) for

30 cycles at 94°C for 30 seconds, at 60°C for 30 seconds, and at 72°C for 1 minute. The amplified products are cloned into the PCRII T-A vector (Invitrogen Corp., San Diego, CA).

RT assays. The RT assays are conducted as described in Wilson et al. (1994) and Wilson et al. (1998) and are optimized for the detection of PERV RT as reported by Phan-Thanh et al. (1992). Pelleted virions or virions in cleared supernatant are treated in solubilization buffer (25 mM NaCl, 0.20% Triton X-100, 10 mM Tris, pH 7.5) for 15 minutes at ambient temperature. The solubilized samples are incubated for 3 hours at 37°C in 2X substrate buffer (50 mM Tris, pH 7.5, 10 mM dithiothreitol, 0.6 mM $MnCl_2$, 10 µg of poly (rA)-poly $(dT)_{12-18}$ (Pharmacia, Piscataway, NJ) per ml, and 10 µCi of ^3H[TTP] per 25 µl (22 Ci/mmol). The incubation is terminated with EDTA followed by blotting the synthesized DNA on a DEAE filtermat (LKB-Wallac, Gaithersburg, MD) through use of a harvesting apparatus (Skatron, Sterling, VA) with a rinse of 1% Na_2HPO_4 (pH 7.0) containing 1 mM EDTA. Radioactivity is then determined via liquid scintillation. All samples are assayed in triplicate.

RNase protection assays (RPA). RNA from viral particles or cells is extracted using RNAzol™ B (Tel-Test, Inc., Friendswood, TX). RPA are done with the RPA II Ribonuclease Protection Assay Kit (Ambion, Inc., Austin, TX). Antisense riboprobes are synthesized in the presence ^{32}P[UTP] using the RNA Transcription Kit (Stratagene, La Jolla, CA). In standard RPA conditions, labeled riboprobe (5×10^5 cpm) is incubated with the RNA at 50°C overnight. The annealed reaction is digested with an RNase A/T1 mix at 30°C for 45 minutes. The samples are cleaned up and fractionated on 6% acrylamide-7.6 M urea gels, dried and exposed to Kodak X-OMAT film.

Western analysis. Virion proteins were isolated and separated on 12% SDS polyacrylamide gels. The proteins were transferred to nitrocellulose filters with an Enprotech blotting apparatus (Integrated Separation Systems, Hyde Park, MA). The filters were blocked in phosphate-buffered saline with 10% nonfat dry milk (wt/vol) for 1 hour at ambient temperature. The blocked filters were drained and incubated with a 1:1000 of goat anti-GALV CA or goat anti-SSAV CA antisera in rinse buffer (100 mM NaCl, 10 mM Tris, pH 8, 1 mM EDTA, 0.1% Tween 20) containing 1% nonfat dry milk for 1 hour at ambient

temperature (Biological Carcinogenesis Branch Repository of the National Cancer Institute). The filters were then washed extensively in rinse buffer, and incubated with 50 ng/ml peroxidase-labeled rabbit anti-goat IgG (H + L) (Kirkegaard and Perry, Gaithersburg, MD) in rinse buffer with 1% nonfat dry milk for 1 hour at ambient temperature. The filters were washed and the protein-antibody-peroxidase complexes detected with the Western Blot Chemiluminescence Reagent (DuPont NEN, Boston, MA). The filters were exposed to Kodak X-OMAT film.

Results

Host Range of PERV Isolates

Primary PBMC were isolated from an NIH miniature pig and exposed to two different combinations of mitogens: phytohemagglutinin (PHA) and phorbol myristate acetate (PMA) or PMA and the calcium ionophore A23187. Mitogenic activation by either treatment resulted in a sharp increase in reverse transcriptase (RT) activity levels five days after stimulation (Figure 1A). To determine if the increase in RT activity correlated with the production of infectious virus, stimulated PBMC from NIH and Yucatan minipigs were cocultured with the pig ST-IOWA cell line, a line that does not produce significant endogenous RT activity levels in the supernatants but is susceptible to PERV infection. Both cultures produced detectable RT activity 14 days after exposure to activated PBMC (Figure 1B). These results indicated that mitogenic activation of the pig PMBC released PERV capable of productive infection of pig cells. To determine if the produced PERV can infect human cells, stimulated PBMCs were cocultured with the human embryonic kidney 293 cell line. RT activity was detected in 293 cells at day 31 (Figure 1C) and continued to increase to levels comparable to RT activity levels produced by infected ST-IOWA cells. These results clearly demonstrated that the stimulated pig PBMC produce PERV that can productively infect human cells. These findings suggest that the stimulation of porcine lymphocytes, transferred to the patient in a xenograft, may result in the production of replication-competent human-tropic PERV capable of infecting the patient.

In order to test if the PERVs of this primary 293 infection (1°-293/PERV) could improve their infection efficiency in human cells, supernatant

from the 1°-293/PERV culture was passaged into a new culture of human 293 cells (2°-293/PERV) and allowed to spread through the culture (Figure 2). After the culture reached maximum RT activity, supernatant from the 2°-293/PERV culture was passaged into fresh 293 cells and allowed to spread (3°-293/PERV). The titer of the PERVs produced by these three cultures was quantitated by generating MLV-βgal pseudotypes.

The titers of all three PERV cultures were approximately the same on the control ST-IOWA cells (Figure 3). However, the titers of the MLV-βgal/PERV pseudotypes produced from the 2°-293 and 3°-293 cultures were 5-fold higher compared to the 1°-293 culture. The relative copy number of integrated PERV proviruses in these three PERV infected 293 cultures was quantitated by Southern analysis. As shown in Figure 4, the DNA isolated from the 2°-293/PERV and 3°-293/PERV cultures contained more integrated PERV proviruses per cell relative to the DNA of the 1°-293/PERV cultures.

Overall, the host range of the PERVs produced from the 293/PERV cultures appears to coincide with a PERV-A related isolate (see Table 4 compared to Takeuchi et al., 1998). One notable exception is the inability of PERV-1.15 MLV-βgal pseudotypes to infect D17 cells, suggesting that the changes in the envelope glycoproteins may have altered the host range.

Table 4. Host range of PBMC PERV produced by 293 cells

Species	Cell	Titer of *LacZ* pseudotype[a] 1°	2°	3°
Human	HeLa	+	+	+
	HOS	+	+	+
	Caki-1	-	-	+
	293	+	++	++
Primate	FRhK-4	-	-	-
Pig	ST-IOWA	++	++	++
	1o PT	+	+	+
Dog	D17	-	-	-
Rabbit	SIRC	-	-	-
Hamster	E36	-	-	-
Mink	Mv-1-Lu	++	++	++
	MiCl1	+	++	++
Cat	Fc3Tg	+	+	++
	AK-D	+	+	++
	CRFK	++	++	++
	PG4	++	++	++

[a] MLV-βgal pseudotypes were produced in the PERV infected human 293 cultures: negative (-); 1-100 BFU/ml (+); >100 BFU/ml (++).

Table 5. Productive infection of human and animal cell lines by 293/PERV

Cell Line	Virus[a]	*LacZ*[b]	RT[c]	RT-PCR[d]
ST	1°	++	neg	nd
(pig testis)	2°	++	d.9	nd
	3°	++	d.9	nd
293	1°	+	d.18	nd
(human kidney)	2°	++	d.10	nd
	3°	++	d.10	nd
Caco-2	1°	?	neg	–
(human colon)	2°	?	neg	–
	3°	?	d.18	–
HepG2	1°	++	neg	–
(human liver)	2°	++	d.26	+
	3°	++	d.26	+
HT1080	1°	+	neg	–
(human fibrosarcoma)	2°	++	d.26	+
	3°	++	d.13	+
Mv-1-Lu	1°	+	neg	+
(mink lung)	2°	++	d.21	+
	3°	++	d.38	+
CRFK	1°	+	neg	+
(cat kidney)	2°	+	d.14	+
	3°	++	d.14	+

[a] Culture supernatant from 1°, 2°, or 3° –293/PERV cells.

[b] Titer of MLV-βgal pseudotype: negative (–); 1-100 BFU/ml (+); >100 BFU/ml (++).

[c] The day when the RT activity was greater than 2-fold over background activity from uninfected cells. The assay was terminated after 8 weeks.

[d] At 8 weeks postinfection, RNA was isolated from the culture supernatant and assayed for *pol* sequences by RT-PCR.

nd Not determined.

? High background staining made the data uninterpretable.

PERV Produced by the 293/PERV Cultures Can Productively Infect Other Human, Mink and Cat Cell Lines. A number of different cell lines were employed to determine the tissue and species specificity of PERV produced by 293/PERV cultures (Table 5). All the cell lines tested except Caco-2 were productively infected by the virus populations produced by the 2° and 3°–-293/PERV cultures. The 3°–293/PERV infected Caco-2 culture produced RT

activity at day 18 and detectable *pol* RNA by RT-PCR indicating a productive infection. The 1°-293/PERV culture produces 5-fold lower PERV titers (see Figure 3) which may account for the lower replication efficiency in most lines. The transfer of significant levels of replication-defective PERV genomes into the primary 293 cells may account for the lower titers. The ability of the PERV produced by the 2° and 3°-293/PERV cultures to efficiently replicate in most cultures may be the result of the loss of defective interfering PERV genomes or the adaptation of the virus, or both.

An expanded analysis of species tropism indicated that cell lines derived from mouse, rat, rabbit, dog, cow, and rhesus monkey were resistant to infection by 293/2° pseudotypes, while cell lines from cat or mink cell lines were susceptible. This latter susceptibility was low compared to 293 cells, with the exception of MiCL and PG4 cell lines. Mink and cat cell lines were also infected with PERV infected 293/2° supernatant. Only low levels of RT activity were observed in MiCL and CRFK cultures. PG-4 cultures had RT activity of 933 cpm [^{3}H-TTP] at 3 weeks, which was reduced to 2344 cpm by 5 weeks, post infection.

Analysis of the Susceptibility of Hematopoietic Cells to Infection by PERV. In order to assess whether primary human PBMC (hPBMC) were susceptible to infection by PERV, PHA-activated hPBMC were cocultured with irradiated 293/2° virus-producer cells and maintained in IL-2-containing medium for 8 weeks. No RT activity above background levels or viral RNA as measured by RT-PCR were produced during the course of the experiment. Since maintenance of the hPBMC in IL-2 during the course of the experiment biases the culture conditions towards the proliferation of T cells, other hematopoietic lineages that may be susceptible to infection may not have been represented. To investigate the possibility that other hematopoietic lineages may be permissive for infection, a number of human hematopoietic cell lines representing the T cell, B cell, myeloid, and NK cell lineages were analyzed for their susceptibility to PERV infection by coculture with irradiated 293/2° virus producer cells. Supernatants from the cocultures containing either M14 (T cell lineage), Jurkat (T cell lineage), K562 (myeloid lineage), or the NK cell line YTN10, remained negative for RT activity during the 8 week course of the experiment, although

viral RNA could be detected by RT-PCR throughout the experiment. Figure 5 shows the data from the RT activity for the cocultures containing the T cell line Molt 4, the B cell lines Daudi and Raji, and the myeloid cell line U937. By 4 weeks post-coculture, the RT activity in the Molt 4- and Daudi-containing cocultures was positive and continued progressively to increase throughout the period of the coculture. In contrast, the RT activity for both the Raji and U937 sets of cocultures plateaued by 4 weeks post-culture. The results from this experiment suggest that the Molt 4, Daudi, Raji, and U937 cell lines were permissive for productive infection by PERV.

The RT positive hematopoietic cell lines were then co-cultured with primary hPBMC, as a virus population may have been selected in the susceptible hematopoietic cell lines that could more efficiently infect primary hematopoietic cells. The irradiation conditions optimal for lethal irradiation were determined for each of the RT positive Daudi, Molt 4 and U937 cell lines. Then lethally-irradiated RT-positive Daudi, Molt 4 and U937 were each employed as virus-producer cells in cocultures with primary hPBMC activated with PHA or with human 293 cells as positive controls. By 2 weeks post-coculture, each of the cocultures containing 293 cells as target cells became significantly RT positive (>7,000 cpm), and by 3 weeks, the RT activity in each of these cultures increased to >20,000 cpm. By contrast, none of the cocultures containing the hPBMC demonstrated RT activity higher than negative control cultures over the course of the experiment. Although viral RNA was detected by RT-PCR in the supernatant of cultures sampled 1-2 weeks post-exposure, the supernatant was negative for viral RNA by RT-PCR by three weeks and remained so out to the 8-week time point. The positive RT-PCR results obtained at the early time points most likely reflect presence of residual irradiated virus-producer cells which disappear from the culture at the later time points, rather than infected cells.

Table 6. Comparison of the nucleotide and deduced amino acid sequence of PERV-1.15 with the three known PERV *env* subgroups.

	1.15	A	B	C
PERV-1.15	-	96	85	73
PERV-A	97	-	82	76
PERV-B	87	84	-	70
PERV-C	72	76	72	-

Amino Acid Identity (%)

Nucleotide Identity (%)

Env Subgroups of PERV in PERV- infected 293 Cultures

To determine what PERV envelope subgroups were present in virions produced by the 293/PERV populations, the envelope regions was cloned by RT-PCR amplification of virion RNA isolated from 1°, 2°, and 3°-293/PERV supernatants. The primers used for RT-PCR were designed from the PERV-A and PERV-B envelope sequences. Oligonucleotide primers were synthesized homologous to a conserved region at the 3′-end of the *pol* gene (5′ of the PERV *env* gene) and a conserved untranslated region 3′ of the *env* gene. The amplified products were cloned into the pCRII T-A cloning vector (Invitrogen) and representative clones sequenced from each culture. Unexpectedly, only one PERV envelope gene species was detected in virions produced from all three cultures. The deduced amino acid sequence shows that the surface glycoprotein region of the gene is almost identical to PERV-A, but the transmembrane glycoprotein region of the gene is almost identical to PERV-C (Figure 6). The nucleotide and amino acid sequence homologies of PERV-1.15 with PERV-A, -B, and -C are summarized in Table 6.

While the PERV-1.15 envelope gene is clearly in the PERV-A receptor subgroup family, the gene contains a unique transmembrane glycoprotein that may be important for efficient PERV replication in human cells. The variation in the PERV *env* genes may be significant since variant MLV *env* genes have

been shown to not only broaden the host range of the esotropic MLV but increase the pathogenicity (Rosenberg et al., 1997). These viruses arise by recombination between different endogenous MLVs. Recombination between *env* sequences of exogenous and endogenous feline leukemia viruses (FeLV) also occurs in FeLV-induced thymic tumors.

All 293/PERV cultures contained PERV-A envelope sequences as determined by PCR using subgroup-specific envelope primers. However, PERV-B envelope sequences were not detected in the 293/PERV culture DNAs. The PERV-C envelope sequence was detected in the 1°-293/PERV culture, but not in the subsequent virus passages. PERV-C does not infect most human cells efficiently.

Isolation of Other Human-Tropic PERVs. To identify other human-tropic PERV, primary cell cultures, e.g., pig aortic endothelial cells (PAEC from, for example, NIH and Yucatan minipig breeds), pig PBMC, and primary pig hepatocytes, from normal pig tissues are assayed for the production of human-tropic PERVs on human 293 cells. The cultures are passaged and monitored for PERV production by RT-PCR and RT activity. The PERV populations are passaged onto fresh human cells to generate secondary cultures to determine if a particular PERV species dominates, and if the overall replication efficiency improves. Env subgroups and LTR-U3 sequences are determined as described above.

New preparations of PERV cDNA are synthesized by RT-PCR from virion RNA isolated from PERV sources, and 1°, 2°, and 3°-293/PERV culture supernatants. The region from the virion mRNA polyA tail to the PERV *pol* gene is amplified by RT-PCR. The RT-PCR reactions use a *pol* primer that hybridizes just 5′ of the *env* gene, and a second reaction using a *pol* primer homologous to the RT active site region. Two reactions that use different *pol* primers increase the chance of amplifying all PERV variants. ProSTAR Ultra High Fidelity (HF) RT-PCR System (Stratagene) is employed for RT-PCR as it combines high fidelity with long target amplification using the *PfuTurbo* DNA polymerase. *PfuTurbo* DNA polymerase efficiently generates blunt ends. The product is cloned into PCR-Script (Stratagene) designed for blunt-end cloning. This approach does not rely on specific restriction sites to be present in the

~~PERV sequence, and produces cDNA clones that contain both the envelope gene~~ and the U3 LTR region.

The resulting bacterial colonies are grouped first by envelope subgroups by probing colony lifts on nitrocellulose with ^{32}P-labeled DNA probes specific for each PERV envelope subgroup. These regions only detect the variable region of the envelope surface glycoprotein. The probing colony lifts with a specific ^{32}P-labeled probe (DNA region or oligonucleotide), by PCR with specific primers designed to identify the variant sequence, and/or by Southern blots of digested plasmid clone DNA probed with a specific ^{32}P-labeled probe. In this way, thousands of colonies are easily probed for specific PERV sequences, thereby increasing the detection of rare PERV RNAs. For example, PERV-B was not detected in the DNA in any of the 293/PERV cultures, and PERV-C was barely detected in the DNA of 1°-293/PERV. Thus, PERV-B and PERV-C envelope sequences may be represented in virions, especially in virions produced by PBMC and the 1°-293/PERV culture supernatants. RT-PCR reactions designed to amplify only PERV-B and PERV-C mRNAs are also done. Finally, the expression profile of PERV envelope and U3-LTR sequences in PBMC is analyzed by RNAse protection assays. Specific PERV envelope and U3-LTR sequences are cloned into pBluescript KS (Stratagene), and used to produce ^{32}P-labeled antisense RNA probes. Pig and human GPDH probes are also used to normalize RNA levels in the assays for quantitation of PERV RNA levels in PBMC. These assays determine if PERV-B and PERV-C loci are expressed in PBMC. The nucleotide sequence is then determined for 10-15 representative clones of each unique PERV group.

Cellular DNA is probed, by Southern analysis and PCR, for the presence of any new or variant PERV sequence identified by these experiments. This analysis verifies that the PERV sequence is present in the genome, and not an artifact of the cloning or analysis procedure, although the sequence could be the result of adaptation. The biological properties of all PERV sequences is characterized in an infectious molecular clone. RNase protection assays are used to identify and quantitate the expression levels of the unique PERV elements in RNA isolated from a variety of tissues: brain, pancreas, spleen, liver, heart, kidney, muscle, lung, and PBMC.

~~Example 3~~

Molecular Cloning and Characterization of PERVs

A lambda genomic library was prepared from *Sau*3A-partially digested DNA isolated from 2°-293/PERV cells in the Lambda Dash II vector (Stratagene). The library was probed with a ^{32}P-labeled PERV *pol* gene fragment, and ten genomic clones isolated. Six of the clones were unique and contained partial PERV proviruses.

All of the cloned PERV regions were nearly identical, with at most two amino acid changes in the coding regions, except the PERV sequences in lamA8 (Figure 7). The lamA8 *pol* gene contains an 86 nucleotide deletion that results in the truncation of the open reading frame at amino acid 887, a loss of 308 amino acids. The lamA8 *env* gene contains 101 nucleotide insertion that results in the truncation of the open reading frame at amino acid 599, a loss of 60 amino acids which includes the putative transmembrane region of the transmembrane glycoprotein. It is unlikely, therefore, that lamA8 contains a functional *pol* or *env* gene.

The PERV regions cloned from the 2°-293/PERV culture were compared to the putative complete PERV cDNA, PERV-MSL (Akiyoshi et al., 1998), the PERV-A (Letissier et al., 1997) and PERV-1.15 envelope genes, and gibbon ape leukemia virus (GALV) (Table 7). The 293/PERV *gag* and *pol* genes, as well as the 5′ and 3′ untranslated regions were nearly identical to the PERV-MSL nucleotide and deduced amino acid sequence.

Table 7. Comparison of the 2°-293/PERV regions contained within the lambda clones with other PERV isolates

Region	Sequence[a]	Percent Identity PERV-MSL[b]	PERV-A	PERV-1.15	GALV[c]
LTR	N	78			
5′-ut	N	97			
gag	N	98.9			
	A	98.5			62.6
pol	N	99			
	A	99			68
env	N	86.7	97	99.8	
	A	85	96	99.7	47
3′-ut	N	100			

[a] N, nucleotide sequence; A, amino acid sequence.
[b] PERV-MSL, a putative full-length PERV cDNA clone with the C-type envelope gene.
[c] GALV, gibbon ape leukemia virus.
ut untranslated region.

The *env* gene in lamA6 has 4 nucleotide and 2 amino acid differences with PERV-1.15, the 293/PERV *env* gene cloned by RT-PCR from virion RNA (Figure 18). Upon comparing the nucleotide sequence of the 293/PERV and PERV-MSL LTRs, a large divergence was observed in the U3 region (Figure 8). The 293/PERV LTR contains 71 more nucleotides than the PERV-MSL LTR. The sequence of the PERV sequences in Lambda clones A1, A11, A3A, A10, and A8 is also shown in Figure 18.

Two recombinant PERV proviruses were prepared to test if they produce infectious virus in 293 cells. The constructs, an A3A/A6 chimera and an A1/A6 chimera, are outlined in Figure 9. All constructs were built in the pBluescript KS vector (Stratagene), and used the unique BspEI site in the *pol* gene to link the 3′-half of the genome contained in lam A6 to the 5′-half of the genome contained in either lamA1 or lamA3A. A minimum of genomic sequence was cloned with the PERV region: A1, about 1000 bp; A3A, about 30 bp; A6, about 700 bp.

Example 4

Preparation and Detection of Anti-PERV Antibodies

Rabbit polyclonal antisera is produced against 2°-293/PERV virion proteins and against 2°-293/PERV capsid proteins. The 2°-293/PERV cultures produce a relatively large amount of viral particles as demonstrated in Figure 10A. Goat anti-SSAV CA and goat anti-GALV CA antisera easily detect PERV Gag proteins on a Western blot with only minor cross-reaction to control 293 cell supernatant proteins (Figure 10B). These antisera are used as positive controls for the characterization of the anti-PERV antisera and monoclonal antibodies. The 2°-293/PERV cultures produce approximately equal amounts of the p30 capsid (CA) protein in 5 ml of supernatant as ALV infected cultures produce ALV p27 CA protein (lanes 2 and 5). The high-titer ALV stock contained 10^7 iu/ml. The 2°-293/PERV virions are collected and purified by equilibrium density centrifugation on sucrose gradients. The banded virions are collected, dialyzed, and used for antibody production. The PERV CA protein is isolated from SDS-PAGE gels (Figure 10A) and also used for polyclonal antisera production.

Two rabbits are used for each antigen preparation. The antigen (100 μg) mixed in Complete Freund's Adjuvant is used for the initial inoculation. The animal is boosted with 50 μg antigen in Incomplete Freund's Adjuvant on day 14, 21 and 49 after the initial inoculation. The route of injection is normally subcutaneous and/or intramuscular at multiple sites. Test bleeds are drawn on day 35 and 56 and screened against PERV proteins by Western blot and immunoprecipitation assays.

Purified PERV CA protein is used to produce mouse hybridomas that secrete monoclonal antibodies against PERV CA. The PERV capsid protein, purified from polyacrylamide gels, is used as the antigen. Five Balb/c mice are injected intraperitoneally or subcutaneously with 400 μg antigen (per mouse) in Complete Freund's Adjuvant and boosted two weeks later with 250-500 μg of the antigen in Incomplete Freund's Adjuvant. All five mice are then tested for the presence of PERV anti-capsid antibodies by Western blot. One of the positive mice is used for hybridoma preparation. Spleenocytes and/or lymph node cells are removed and fused to non-immunoglobulin secreting myeloma

cell line F/O. Hybridomas are screened and positive hybrids are cloned and then subcloned to obtain monoclonal antibody (MoAb) producing cell lines. The hybridomas are screened by both Western blot and immunoprecipitation of PERV capsid protein. The MoAb cell lines are isotyped and cryopreserved. MoAbs are purified from the cell line supernatant by protein A/G column chromatography.

The new anti-PERV antibodies, as well as the anti-SSAV and anti-GALV CA antisera, are tested for their ability to detect PERV proteins in live and fixed PERV infected cells. An immunofluorescence and/or immunohistochemical assay for PERV infection simplifies the detection of PERV infection and allows the direct quantitation of PERV titers.

To detect anti-PERV antibodies in sera, a Western-based assay system is employed. Protein preparations made from PERV virions produced by the 2°-293/PERV culture are separated by SDS-PAGE and transferred to nitrocellulose filters. Virion protein extracts are used for two reasons. First, PERV produced by human cells does not display the α-Gal xenoreactive carbohydrate that may bind to the α-Gal antibodies in human sera. Second, the 2°-293/PERV culture produces high levels of PERV virions as shown by analysis of PERV virion protein extracts. Goat anti-SSAV and anti-GALV CA antisera that cross-reacts with the PERV CA protein is employed. The 2°-293/PERV virions are purified by equilibrium centrifugation on sucrose gradients. In one embodiment, the assay employs peroxidase-conjugated secondary antibodies and enhanced chemiluminescence (Amersham, Pharmacia Biotech, Piscataway, NJ) to detect antibodies bound to the PERV proteins. To determine what effect human sera may have on the performance of the assay (e.g., alter the antibody sensitivity or cross-reaction with common human antibodies), the anti-CA antisera is added to dilutions of control human sera (1:10, 1:50, 1:100) and tested.

Serum samples from at least 300 pig slaughterhouse workers, plus controls, are screened. Control samples, including sera from a patient with little or no exposure to pigs, and sera from two populations of retrovirus-infected patient populations (50 HIV-1; 20 HTLV-1) is used to evaluate the specificity of antibody binding to PERV and non-PERV proteins. Preparative single well SDS-PAGE is used to separate the PERV virion proteins, and the proteins

transferred to a nitrocellulose filter. The Miniblotter II apparatus (Immunetics, Cambridge, MA) permits the screening of 45 different samples by dividing the Western blot into 45 sample cells. A negative control serum and a positive control serum (human sera with SSAV or GALV anti-capsid antisera) is assayed with each blot. A 1:50 dilution of the serum samples is screened initially. Human blood samples are also tested for PERV nucleic acid and anti-PERV antibodies.

Example 5

Soluble Forms of the Subgroup A Avian Leukosis Virus Receptor Tva Significantly Inhibit ALV(A) Infection *in vitro* and *in vivo*

Three cell surface proteins have been identified as ALV receptors: Tva, the receptor for ALV(A) (Bates et al., 1998; Bates et al., 1993; Young et al., 1993); CAR1, the receptor for ALV(B) and ALV(D) (Brojatsch et al., 1996; Smith et al., 1998); and SEAR, the receptor for ALV(E) (Adkins et al., 1997). To aid in the characterization of the interactions between Tva and ALV(A) envelope glycoproteins, soluble forms of the 83 amino acid extracellular domain of the Tva receptor protein (sTva) were constructed by Young and colleagues (Connolly et al., 1995), who reported that pre-incubation of the sTva proteins with different envelope subgroup ALVs caused a specific block to infection of susceptible chicken cells by ALV(A), but had no effect on ALV(B) or ALV(C) infection.

To determine if cells and chickens expressing sTva proteins are resistant to ALV(A) infection, ALV-based replication-competent retroviral vectors were used to efficiently deliver and express *stva* genes (Federspiel et al., 1997). The vectors are available with five different envelope subgroups (A-E) which enables multiple genes to be delivered and expressed in virtually every cell.

Materials and Methods

Soluble receptor and retroviral vector constructs. The two soluble receptor gene constructs, contained in the plasmids pLC126 and pKZ457, were gifts of John Young (Harvard Medical School). The pLC126 *stva* gene (Connolly et al., 1994; Hughes et al., 1987), encoding the 83-amino-acid Tva extracellular domain fused to a 9-amino-acid antibody epitope tag derived from

influenza virus hemagglutinin, followed by six histidine residues, was isolated as a *Nco*I-*Pst*I fragment and cloned into the *Nco*I and *Pst*I sites of the CLA12NCO adaptor plasmid (Federspiel et al., 1997; Hughes et al., 1987). The pKZ457 *stva-mIgG* gene, encoding the 83-amino-acid Tva extracellular domain fused to the constant region of the mouse IgG heavy chain (nucleotides 353-1072) (Tucker et al., 1979), was isolated as a *Nco*I-*Blp*I fragment. The *Blp*I site was made blunt and the modified fragment was cloned into the *Nco*I and *Sma*I sites of CLA12NCO. Both the *stva* and *stva-mIgG* genes had been modified to contain *Nco*I sites at their initiator ATGs. The soluble receptor gene cassettes were isolated as *Cla*I fragments from the adaptor plasmids and cloned into the unique *Cla*I site of the RCASBP, RCAS, and RCOSBP retroviral vectors with subgroup (B) and subgroup (C) envelope genes. The RCAS family of replication-competent retroviral vectors have been described (Federspiel et al., 1994; Federspiel et al., 1997; Hughes et al., 1987; Petropoulous et al., 1991; Petropoulous et al., 1992).

The *stva-mIgG* gene isolated as a *Cla*I fragment from the CLA12NCO adaptor plasmid was subcloned into the TFANEO expression vector (Federspiel et al., 1989). TFANEO is a companion expression vector to the RCAS family of retroviral vectors. The expression cassette of TFANEO consists of two LTRs derived from the RCAS vector that provide strong promoter, enhancer, and polyadenylation sites flanking a unique *Cla*I insertion site. The TFANEO plasmid also contains a *neo* resistance gene expressed under the control of the chicken β-actin promoter, and an ampicillin resistance gene for selection in *E. coli*.

The RCASBP(A)AP, RCASBP(C)AP and RCASBP(C)AP retroviral vectors which contain the heat-stable human placental alkaline phosphatase gene (AP) have been described (Federspiel et al., 1997; Field-Berry et al., 1992; Fekete et al., 1993). The AP gene, contained on a *Sal*I fragment, was cloned into the *Sal*I site of the CLA12 adaptor plasmid, and then subcloned into the RCASBP vectors as a *Cla*I fragment (gift of Constance Cepko).

Cell culture and virus propagation. Chicken embryo fibroblasts (CEFs) derived from 10-day, line 0 embryos (C/E) (Astrin et al., 1979) were grown in DMEM (GIBCO/BRL) supplemented with 10% tryptose phosphate broth

(GIBCO/BRL), 5% fetal bovine serum (GIBCO/BRL), 5% newborn calf serum (GIBCO/BRL), 100 units of penicillin per ml, and 100 µg of streptomycin per ml (Quality Biological, Inc., Gaithersburg, MD) as previously described (Federspiel et al., 1997). DF-1 cells were grown in DMEM supplemented with 10% fetal bovine serum, 100 units of penicillin per ml, and 100 µg of streptomycin per ml (Himly et al., 1998; Schaefer-Klein et al., 1998). Both CEF and DF-1 cultures were passages 1:3 when confluent.

Virus propagation was initiated by calcium phosphate transfection of plasmid DNA that contained the retroviral vector in proviral form (Federspiel et al., 1997). In standard transfections, 5 µg of purified plasmid DNA was introduced into DF-1 cells or early passage CEF by the calcium phosphate precipitation method (Kingston et al., 1989). Viral spread was monitored by assaying culture supernatants for ALV capsid protein by either Western transfer analysis or ELISA (Smith et al., 1979). Virus stocks were generated from the cell supernatants. The supernatants were cleared of cellular debris by centrifugation at 2000 × g for 10 minutes at 4°C and stored in aliquots at -80°C. DF-1 cells transfected with the TFANEO plasmid were grown in 500 µg/ml G418 (Gibco/BRL) to select for neomycin-resistant cells. Clones were isolated using cloning cylinders (Bellco Glass Inc., Vineland, NJ), expanded, and maintained with standard medium supplemented with 250 µg/ml G418.

ALV alkaline phosphatase challenge assay. In a direct AP challenge assay, CEF or DF-1 cell cultures (about 30% confluent) were incubated with 10-fold serial dilutions of the RCASBP/AP virus stocks for 36-48 hours at 39°C. In a pre-absorption AP challenge assay, the 10-fold viral serial dilutions were first mixed with 2 ml of supernatant containing sTva-mIgG for 3 hours at 4°C, and then assayed as above. The assay for alkaline phosphatase activity was modified from procedures of Cepko and co-workers (Federspiel et al., 1994; Fekete et al., 1993; Fields-Berry et al., 1995). Cells were fixed in 4% paraformaldehyde in Dulbecco's phosphate-buffered saline (PBS) for 30 minutes at 25°C, washed twice in PBS for 5 minutes each, and incubated for 1 hour at 65°C to inactivate endogenous AP activity. The cells were then washed twice with AP detection buffer (100 mM Tris•Cl, pH 9.5/100 mM NaCl/50 mM $MgCl_2$) for 10 minutes and exposed to the AP chromogenic substrates nitroblue tetrazolium (300 µg/ml)

and 5-bromo-4-chloro-3-indoyl phosphate (170 µg/ml) (GIBCO/BRL). Enzymatically active AP produces an insoluble purple precipitate. The reaction was stopped by the addition of 20 mM EDTA, pH 8.0 in PBS.

Immunoprecipitation and Western transfer analysis of stva-mIgG proteins. A 500 µl aliquot of culture supernatant or serum was incubated with 50 µl of anti-mouse IgG-agarose beads (Sigma) for ≥ 1 hour at 4°C. The sTva-mIgG agarose bead complexes were collected by centrifugation and washed twice in dilution buffer [50 mM Tris-buffered saline (TBS), 1% Triton X-100, 1 mg/ml BSA], once in 50 mM TBS and once in 0.05 M Tris•Cl, pH 6.8. The washed complexes were collected by centrifugation, resuspended in 50 µl 1X Laemmli buffer (2% SDS, 10% glycerol, 0.05 M Tris•Cl, pH 6.8, 0.1% bromophenol blue) without β-mercaptoethanol, and heated for 5 minutes at 100°C. The agarose in the samples was collected by centrifugation for 2 minutes and the supernatants were transferred to new tubes. Prior to gel electrophoresis, 1.0 µl β-mercaptoethanol was added to each 50 µl sample and the samples were heated for 5 minutes at 100°C. The denatured immunoprecipitates were separated by 12% SDS-PAGE, and transferred to a nitrocellulose membrane. The filters were blocked with 10% non-fat dry milk (NFDM) in PBS, probed with 0.05 µg/ml peroxidase-conjugated goat anti-mouse IgG antibodies (Kirkegaard and Perry laboratories, Gaithersburg, MD) in rinse buffer (100 mM NaCl, 10 mM Tris•Cl, pH 8, 1 mM EDTA, 0.1% Tween 20) and 1% NFDM, and washed in rinse buffer. Protein/antibody complexes were detected with the Western Blot Chemiluminescence Reagent (NEN) according to the manufacturer's instructions. The immunoblot was then exposed to Kodak X-Omat film.

In vivo ALV challenge assay. Line 0 embryos were somatically infected with RCASBP(B), RCASBP(B)stva, or RCASBP(B)stva-mIgG by injecting unincubated eggs near the blastoderm with 100 µl containing 1×10^6 CEF or DF-1 cells producing the virus. Line 0 is a White Leghorn line that is genetically susceptible to all ALV subgroups except subgroup (E) and is free of endogenous proviruses that are closely related with ALV (Astrin et al., 1979). Viremic chicks were identified at hatch by ELISA for the ALV capsid protein p27. Viremic and uninfected control chicks were infected intra-abdominally

with 10^5 infectious units of either RAV-1 [an ALV(A) isolate] or RAV-49 [an ALV(C) isolate]. Blood was collected at 2, 4 or 9 weeks post-challenge, and the serum assayed for infectious subgroup (A), (B), or (C) ALV by the *in vitro* ALV Assay (see below).

In vitro ALV assay. The presence of infectious ALV in chickens was determined by assaying the serum samples on a panel of cell lines with different ALV envelope subgroup susceptibilities. The panel of indicator cell lines included: line 0 CEF (C/E) which supports the replication of ALV(A), ALV(B), and ALV(C); line *alv*6 CEF (C/A) which supports ALV(B) and ALV(C) replication; line RP30B-cell line (C/B) which supports ALV(A) and ALV(C) replication; and line 15.C-12 CEF (C/C) which supports ALV(A) and ALV(B) replication. Serum samples (100 µl) were added to the cells and the cells were incubated for 9 days in media (5% serum) to allow ALV to spread. The media was changed after 3 days to avoid detection of ALV proteins in the original serum sample. The cells were then solubilized by 2 cycles of rapid freeze-thaw to release ALV Gag antigens. The ALV capsid protein was detected by ELISA. A positive sample was defined as having an optical density reading of > 0.200. The *in vitro* ALV Assay can detect infectious ALV titers as low as 10 IFU/ml.

RNase protection assay. Total RNA was isolated from cells in culture, or homogenized tissues of experimental birds, by the RNazol B method (Tel-Test, Inc., Friendswood, TX). Sequence-specific RNA probes were cloned into pBluescript KS as follows: the RAV-1 envelope sequences were cloned as an *Xho*I to *Xba*I fragment (Genbank accession # M19113; nucleotides 248-676) (Bora et al., 1988); the RAV-2 envelope sequences were cloned as a *Bam*HI to *Sal*I fragment (Genbank accession # M14902; nucleotides 612-1080) (Bora et al., 1986); the *stva* probe was generated from an *Eco*RI to *Pst*I fragment from the plasmid pLC126 (Genbank accession # L22752; nucleotides 9-386) (Bates et al., 1993; Connolly et al., 1994); and the *stva-mIgG* probe was generated from a *Cla*I to *Bam*HI fragment derived from the adaptor plasmid construct which contains the 5′-*Cla*I site and transcription leader from the CLA12NCO adaptor plasmid and a synthetic sequence encoding the 83-amino acid Tva extracellular domain from pKZ457 that is different from the *stva* gene. A fragment of the chicken glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene (Genbank

accession # K01458; nucleotides 163-361) (Panabieres et al., 1984) was used as a control for the quantity and quality of the RNA. The constructs were linearized by restriction endonuclease digestion and gel purified. ^{32}P-labeled antisense RNA probes were synthesized using the RNA Transcription Kit (Stratagene, La Jolla, CA). The probes were hybridized with 20 µg of total RNA in 20 µl hybridization solution (80% formamide, 10 mM sodium citrate pH 6.4, 300 mM sodium acetate pH 6.4, 1 mM EDTA) overnight at 42°C. RNase protection assays were performed using the RPA II Ribonuclease Protection Kit (Ambion, Austin, TX). The RNA samples were digested with the RNase A/T1 mixture diluted 1:75. The protected RNA probe fragments were separated on a 6% acrylamide/7.6 M urea gel and exposed to Kodak X-Omat film.

PCR assays. DNA was isolated from cells in culture or tissues of experimental birds using the QIAmp Tissue Kit (Qiagen). Each PCR contained 1.25 µl 10X PCR buffer (final concentration, 50 mM Tris•Cl, pH 8.3, 50 mM KCl, 7 mM $MgCl_2$, 1.1 mM β-mercaptoethanol), 1.25 µl of 1.7 mg/ml BSA, 0.5 µl of each dNTP at 25 mM, 0.5 µl of each primer (A_{260} = 5), 6.0 µl H_2O, and 1.0 µl of DNA (genomic DNA about 100 ng/µl; plasmid DNA about 2 ng/µl). The reactions were heated to 90°C for 1 minute and initiated by the addition of 1.5 µl of Taq DNA polymerase (Promega, Madison, WI) diluted 1:10 v/v (0.75 units). Thirty cycles of PCR were carried out as follows: 90°C for 40 seconds, then 59°C for 80 seconds. Diagnostic primers used to detect ALV(A) *env* (Bora et al., 1988) were 5′-GGGACGAGGTTATGCCGCTG-3′ (SEQ ID NO:24; about 50 bp upstream of *Kpn*I site) and 5′-GGGCGTGCGCGCATTACCAC-3′ (SEQ ID NO:25; nucleotides 871-851), yielding a 937 bp fragment. The PCR extension temperature was increased to 62°C for amplifying ALV(A) *env*. Diagnostic primers used to detect ALV(B) *env* (Bora et al., 1986) were 5′-GACCGACCCAGGGAACAATC-3′ (SEQ ID NO:26; nucleotides 713-732) and 5-ATGAGGAAAATTGCGGGTGG-3′ (SEQ ID NO:27; nucleotides 1141-1122), yielding a 429 bp fragment. Diagnostic primers used to detect *stva* (Bates et al., 1993; Connolly et al., 1994) were 5′-GGAATGTGACTGGTAATGGA-3′ (SEQ ID NO:28; nucleotides 56-75) and 5′-GCCTTAGTGATGGTGATGGT-3′ (SEQ ID NO:29; nucleotides 369-350), yielding a 314 bp fragment. Diagnostic primers used to detect *stva-mIgG* were 5′-CCATCCGTCTTCATCTTCCCT-3′

(SEQ ID NO:30; nucleotides 974-994) and 5′-TGGTGCGGTGTCCTTGTAGTT-3′ (SEQ ID NO:31; nucleotides 1562-1542), yielding a 589 bp fragment of the mouse IgG gene (Tucker et al., 1979). The amplified DNA fragments were separated on 0.8% agarose gels and visualized with ethidium bromide.

Results

Experimental approach. The *stva* and *stva-mIgG* receptor gene fusions were subcloned into the CLA12NCO adaptor plasmid which contains a transcriptional leader sequence and has a consensus ATG start site contained in a *Nco*I site. These sequences work very efficiently with the promoter/enhancer elements of the ALV-based retroviral vectors to express experimental genes at high levels (Hughes et al., 1987). The RCAS family of retroviral vectors were derived from the Schmidt-Ruppin A strain of Rous sarcoma virus (RSV) and were present in proviral form on pBR-based plasmids (Federspiel et al., 1997). Experimental genes were inserted into the vectors in the unique *Cla*I site (which replaces the *src* gene in RSV) and so are translated from a spliced mRNA. Retroviral vectors that carry and express the *stva* and *stva-mIgG* genes are shown schematically in Figure 11. Virus propagation was initiated by transfection of plasmid DNA containing the retroviral vector into avian cells (Figure 12). The culture was then passaged until a maximum viral titer was achieved (6-10 cell passages depending on the vector (Federspiel et al., 1997). Because vectors that use different receptors are available, this system can be used to deliver multiple genes to virtually all cells in the culture (Givol et al., 1994). Cell cultures that express sTva or sTva-mIgG from a subgroup (B) or (C) vector were subsequently challenged with ALV(A) to quantitate the antiviral effect of the sTva proteins.

Antiviral effect of sTva *in vitro* and *in vivo*. The initial experiments testing the effects of soluble receptors on viral replication were done with the sTva protein. The *stva* gene was introduced into the RCASBP vector, which produces the highest titer viral stocks and the highest level of expression of an experimental. To quantitate the antiviral effect of sTva on ALV(A) infection, CEF fully infected with the vector alone [either RCASBP(B) or RCASBP(C)], vectors that express the *stva* gene [RCASBP(B)stva or RCASBP(C)stva] or

uninfected CEF were challenged with RCASBP(A)AP, the subgroup (A) RCASBP vector containing the human placental alkaline phosphatase reporter gene (AP). The results of a representative assay are shown in Table 8. CEF cultures producing sTva, either from RCASBP(B) or RCASBP(C), were > 100-fold more resistant to infection by RCASBP(A)AP than cultures infected with the vector alone. CEF cultures infected by the RCASBP(B) or RCASBP(C) vector alone were 3-5-fold less susceptible to RCASBP(A)AP. The antiviral effect of sTva was specific for RCASBP(A)AP infection, since infection by viruses with other envelope subgroups were not inhibited (Table 8).

Table 8.
Relative resistance of CEF expressing sTVA or sTVA-mIgG to ALV infection.

	Challenge Virus		
	RCASBP(A)AP[a]	RCASBP(B)AP	RCASBP(C)AP
Uninfected CEF	1.5×10^6	2.1×10^5	8.4×10^4
RCASBP(B)	4.3×10^5 (4)[b]	ND[c]	2.0×10^4 (4.2)
RCASBP(B)stva	2.9×10^3 (517)	ND	2.1×10^4 (4.0)
RCASBP(C)	6.0×10^5 (3)	8.3×10^4 (2.5)	ND
RCASBP(C)stva	4.0×10^3 (375)	1.2×10^5 (1.8)	ND
RCASBP(C)stva-mIgG	1.5×10^3 (1000)	8.0×10^4 (2.6)	ND

[a]AP-human placental alkaline phosphatase reporter gene.
[b]The resistance of experimental and control CEF to ALV infection relative to uninfected CEF is given in parentheses.
[c]ND-not done

The CEF cultures infected with RCASBP(B) and RCASBP(B)stva were used to inoculate unincubated line 0 eggs to produce chicks viremic with RCASBP(B) or RCASBP(B)stva. Viremic chicks produced in this manner are tolerant to most ALV antigens since the early embryo was infected. The chicks were challenged with 10^5 infectious units of RAV-1, an aggressive ALV(A) strain, to quantitate the antiviral effect of sTva. Blood samples were collected from representative birds of each group at 2 weeks post-challenge, and from all birds 9 weeks post-challenge. The sera were assayed for ALV(A) and ALV(B) by the *in vitro* ALV Assay. The results of the challenges are summarized in

Table 9. Ninety-six percent of the birds infects with the RCASBP(B) vector alone and then challenged with RAV-1 produced ALV(A) at both experimental time points as expected. However, 95% of the birds infected with RCASBP(B)stva did not produce detectable levels of ALV(A). These results demonstrate that sTva has a strong antiviral effect on ALV(A) infection both *in vitro* and *in vivo*. These results also demonstrate the utility of using vectors with different subgroups *in vivo* since experimental birds could be infected with both the RCASBP(B) vector and RAV-1. However, the level of sTva expression could not be quantitated since neither the hemagglutinin nor the histidine epitope tags included on the sTva protein allowed efficient immunoprecipitation of the protein.

Table 9. Chickens expressing sTva are resistant to ALV(A) infection.

	Virus Subgroup Detected					
	2 Weeks[a]			9 Weeks		
	A&B	B	A	A&B	B	A
Uninfected	0/10	0/10	0/10	0/9	0/9	0/9
RCASBP(B)	9/9	9/9	0/9	6/6	6/6	0/6
RCASBP(B)+RAV-1	10/10	10/10	9/10	15/15	15/15	15/15
RCASBP(B)stva	10/10	10/10	1/10	11/12	11/12	0/12
RCASBP(B)stva+RAV-1	10/10	10/10	0/10	20/20	20/20	1/20

[a]All of the birds in each group were not necessarily assayed at both time points.

Antiviral effect of sTva-mIgG *in vitro*. Although the tagged version of sTva could not be immunoprecipitated efficiently, an sTva immunoadhesin sTva-mIgG can be immunoprecipitated and quantitated. sTva-mIgG consists of the 83-amino acid Tva extracellular domain fused to the constant region of the mouse IgG heavy chain. The *stva-mIgG* gene was introduced into the RCASBP(C) vector. To quantitate the antiviral effect of sTva-mIgG compared to sTva, CEF cultures infected with RCASBP(C)stva-mIgG, RCASBP(C)stva, or RCASBP(C) were challenged with either RCASBP(A)AP or RCASBP(B)AP. CEF expressing sTva-mIgG were about 300-fold more resistant to

RCASBP(A)AP infection compared to cells infected with the vector alone, and 2- to 3-fold more resistant than cells expressing sTva (Table 8). The antiviral effect was specific for ALV(A) since no significant change in susceptibility was observed when the cultures were challenged with RCASBP(B)AP.

ALV replication in a permanent, non-transformed cell line derived from line 0 CEF called DF-1 has been described (Himly et al., 1998; Schaefer-Klein et al., 1998). ALV and ALV-based retroviral vectors replicate and express inserted genes in DF-1 cells at levels similar to CEF, and DF-1 can be used to generate clonal cell lines. The antiviral effect of sTva-mIgG produced in DF-1 cultures infected with RCASBP(C)stva-mIgG (Table 10) was similar to that seen in CEF cultures (Table 8). The sTva-mIgG protein was immunoprecipitated from cell culture supernatants with anti-mouse IgG antibody conjugated to agarose beads and analyzed by Western transfer of SDS-PAGE gels (Figure 13). The immunoprecipitated sTva-mIgG protein migrates as a broad band (50-60 kDa) due to post-translational modification and as a minor about 38 kDa band. The about 38 kDa band is probably a degradation product of sTva-mIgG since both bands appear after immunoprecipitation with an ALV(A) surface glycoprotein immunoadhesin, and the amount of the about 38 kDa band increases after repeated freeze-thaw cycles of the viral supernatants. Stable clonal DF-1 cell lines were generated that express different levels of sTva-mIgG under the control of the TFANEO expression vector. These cell lines do not produce infectious ALV and are resistant to RCASBP(A)AP infection at levels similar to cultures expressing sTva-mIgG from the retroviral vectors. Therefore, chronic ALV infection does not make a major contribution to the antiviral effect obtained.

Relationship between sTva-mIgG expression level and the antiviral effect. The *stva-mIgG* gene was subcloned into the RCAS(C) and RCOSBP(C) retroviral vectors. Previously, it has been reported that the RCAS vector replicates to a 5-15-fold lower titer (depending on envelope subgroup and inserted gene) compared to RCASBP and produces protein at an equivalently reduced level (Federspiel et al., 1994). The RCOSBP vector, which lacks a strong transcription enhancer in the LTR, replicates to about 100-fold lower titer compared to RCASBP and produces lower levels of protein. DF-1 cultures infected with RCASBP(C)stva-mIgG, RCAS(C)stva-mIgG, or RCOSBP(C)stva-

mIgG were challenged with RCSABP(A)AP to determine the antiviral effect of different levels of sTva-mIgG on ALV(A) infection. The results of a representative assay are shown in Table 10. The sTva-mIgG produced by these DF-1 cultures was detected by immunoprecipitation of sTva-mIgG followed by the analysis of the proteins by Western transfer (Figure 13). As expected, cultures infected with RCASBP produced the highest level of sTva-mIgG and the greatest antiviral effect (about 200-fold). Cultures infected with RCAS produced slightly lower levels of sTva-mIgG protein and a lower antiviral effect (about 100-fold). Finally, cultures infected with RCOSBP produced the lowest level of sTva-mIgG protein and a modest antiviral effect (about 15-fold).

Table 10.

Relative resistance of DF-1 cells expressing sTva-mIgG to ALV(A) infection.

	RCASBP(A)AP	Resistance[a]
Uninfected DF-1	3.3×10^6	---
RCASBP(C)	1.3×10^6	3
RCASBP(C)stva-mIgG	5.3×10^3	622
RCAS(C)	6.4×10^5	5
RCAS(C)stva-mIgG	5.7×10^3	579
RCOSBP(C)	9.0×10^5	4
RCOSBP(C)stva-mIgG	5.2×10^4	63

[a]The resistance of the cells to ALV(A) infection was determined by dividing the titer obtained on the control uninfected DF-1 cells by the titer obtained for each experimental group.

The antiviral effect of sTva and sTva-mIgG on ALV(A) infection may represent the minimum antiviral effect attainable *in vitro* as measured by the direct ALV AP challenge assay. The assays were done on subconfluent cell cultures (30%) where the levels of the soluble receptor protein had not accumulated to the levels expressed by a confluent culture. To determine the antiviral effect of higher levels of sTva-mIgG, RCASBP(A)AP was pretreated with supernatants collected from confluent DF-1 cultures infected with RCASBP(B), RCASBP(B)stva-mIgG, RCOSBP(B), or RCOSBP(B)stva-mIgG, and then assayed as before. Preabsorption of RCASBP(A)AP with high levels of

sTva-mIgG significantly increased the antiviral effect compared to a direct assay: RCASBP(B)stva-mIgG pretreatment increased the antiviral effect of the direct assay about 500-fold; and RCOSBP(B)stva-mIgG pretreatment increased the direct antiviral effect about 60-fold.

Delivery and expression of sTva and sTva-mIgG *in vivo*. To characterize the efficiency of RCASBP delivery and expression of the sTva proteins in chickens, unincubated line 0 eggs were injected with CEF producing the RCASBP(B) or RCASBP(C) vectors alone, the vectors with the *stva* gene, or the vectors with the *stva-mIgG* gene. Viremic chicks were identified on the day of hatch by an ELISA assay for ALV capsid protein. The sTva-mIgG protein was immunoprecipitated from serum samples of both RCASBP(B)stva-mIgG and RCASBP(C)stva-mIgG infected birds and visualized by Western analysis (Figure 14). The *stva*, *stva-mIgG*, and RCASBP(B) *env* RNA expression levels in liver, heart, spleen, bursa, thymus, kidney, and muscle tissues of infected birds were analyzed by RNase protection assay. An RNase protection analysis of a representative bird infected with RCASBP(B)stva and a representative bird infected with RCASBP(B)stva-mIgG are shown in Figure 15. Relatively high levels of the *stva* or *stva-mIgG* and ALV(B) *env* RNAs were detected in all tissues assayed, indicating that the inserted genes were delivered and expressed efficiently by the RCASBP(B) vector.

Table 11.
Chickens expressing either sTva or sTva-mIgG are resistant to ALV(A) infection but not ALV(C) infection.

	Virus Subgroup Detected[a]		
	B	A	C
RCASBP(B)+RAV-1	4/4	4/4	
RCASBP(B)stva+RAV-1	5/5	0/5	
RCASBP(B)stva-mIgG+RAV-1	9/9	0/9	
RCASBP(B)+RAV-49	4/4		3/4
RCASBP(B)stva+RAV-49	4/4		4/4
RCASBP(B)stva-mIgG+RAV-49	7/8		6/8

[a]Assays were done 4 weeks after challenge.

Antiviral effect of sTva-mIgG *in vivo*. Chicks infected with the RCASBP(B) vector alone, RCASBP(B)stva, or RCASBP(B)stva-mIgG were split into two groups and challenged with 10^5 infectious units of either RAV-1 (subgroup A) or RAV-49 (subgroup C). Blood was collected from each bird four weeks after challenge, and the serum was assayed for ALV(A), ALV(B) and ALV(C) by the *in vitro* ALV Assay (Table 11). As expected, ALV(B) was detected in virtually all of the birds since the RCASBP(B) vector was used for gene delivery. ALV(A) was not detected in the serum of RAV-1 challenged birds containing the *stva* or the *stva-mIgG* genes. However, ALV(A) was detected in the serum of the birds infected with the RCASBP(B) vector alone and challenged with RAV-1. In contrast, the birds of all three experimental groups were equally susceptible to RAV-49 challenge as shown by the presence of ALV(C) in the majority of the birds. Since 19% of the birds challenged with RAV-49 did not produce detectable levels of ALV(C), the titer of the RAV-49 stock may have been lower than expected. The antiviral effect of sTva and sTva-mIgG was specific for ALV(A), consistent with the proposed mechanism of antiviral action, receptor interference.

Representative birds from each RAV-1 challenged experimental group were analyzed for the presence of ALV(A) and ALV(B) *env*, *stva* and *stva-mIgG*

sequences in RNA and DNA isolated from a variety of tissue samples of each bird. A low level of RAV-1 infection and replication in a subset of tissues may go undetected by the *in vitro* ALV assay due to virus inactivation by the sTva or sTva-mIgG proteins in the serum. Antisense riboprobes and primer sets were developed to specifically detect each target sequence by RNase protection assay and PCR. RNA and DNA were isolated from liver, heart, spleen, bursa, thymus, kidney, and muscle tissue of each bird and analyzed by RNase protection assay and PCR assay. A representative RNase protection assay of RNA of one tissue (bursa) from a bird of each experimental group, and an uninfected control bird, is shown in Figure 16. A representative PCR analysis of DNA isolated form tissues of a RAV-1 challenged bird from each experimental group is shown in Figure 17. RAV-1 RNA and DNA were only detected in tissues of birds infected with the RCASBP(B) vector challenged with RAV-1. Therefore, the expression of sTva and sTva-mIgG significantly reduces, if not eliminates, infection by the ALV(A) strain RAV-1 in chickens.

Discussion

Cells expressing the sTva proteins showed significant resistance to ALV(A) infection, presumably due to the secreted receptor proteins binding the glycoproteins of the invading virion, blocking the interactions of the virus and the membrane bound Tva, a form of receptor interference. Tva has been hypothesized to be necessary and sufficient to mediate ALV(A) entry (Balliet et al., 1998; Bates et al., 1993). Several possible mechanisms could account for the sTva inhibition of ALV(A) entry sTva binding of an ALV(A) surface glycoprotein may lead to an irreversible conformational change in SU and TM. Several studies have shown that sTva binding to purified ALV(A) envelope glycoproteins induces a temperature-dependent conformational change in the glycoproteins, and appears to convert the envelope glycoproteins to a membrane-binding state (Balliet et al., 1999; Damico et al., 1999; Gilbert et al., 1995; Hernandez et al., 1994). Binding of sTva or sTva-mIgG to the envelope glycoproteins on the surface of the virus induces a conformational change in both SU and TM similar to the events leading to fusion of the viral and host cell membranes, and converts SU and TM into a form that is unable to bind Tva on the surface of the cell. A conformational change may also lead to the loss of

some of the SU subunits (Orloff et al., 1993). Finally, sTva may inhibit ALV(A) entry by simply binding to SU and physically blocking the access of membrane bound Tva to the virion. By whatever mechanism(s), the sTva proteins block the entry of ALV(A) into cultured cells and cells and tissues of chickens.

The replication-competent ALV-based retroviral vector experimental system enabled the efficient delivery and expression of the *stva* and *stva-mIgG* genes both in cultured cells and in virtually all the cells and tissues of the chicken. RCASBP(A) and (RCASBP(B), as well as other combinations of ALV retroviral vectors [ALV(B) followed by ALV(A); ALV(C) followed by AVL(A)], can be used in CEF and DF-1 cells *in vitro* and *in vivo*. As reported previously, the replication of some RCASBP(B) viruses in CEF and DF-1 cells, and RCASBP(C) viruses on DF-1 cells, were somewhat cytopathic (Himly et al., 1998; Schaefer-Klein et al., 1998). The cytopathic effect manifests itself as a pause in growth rate (2-6 days), after which the cells recover, divide at a normal rate, and express the viral and experimental proteins. It appears that only the cells that produce high levels of the RCASBP(B) or RCASBP(C) envelope glycoproteins show the cytopathic effects. The replication of subgroup (B) and(C) RCAS and RCOSBP viruses, which replicate to lower titers compared to RCASBP, do not cause detectable cytopathic effects. Chronic infection of CEF and DF-1 cells with an ALV vector results in a low level of resistance to infection by other ALV *env* subgroup vectors (2-5-fold) compared to uninfected cells. This may indicate that while the ALV glycoproteins specifically and efficiently interact with the appropriate receptor resulting in receptor interference, the high level expression of one type of envelope glycoprotein on the cell surface may interfere either directly or indirectly with the ability of other ALVs to interact with their host receptors.

Both the RCASBP(B) and RCASBP(C) retroviral vectors were efficient in generating viremic chicks without detectable pathologic effects in short term infections, and the infected chicks expressed relatively high levels of sTva-mIgG protein in their serum. Chicks infected with RCASBP(B) were also efficiently infected with ALV(A). The RCASBP(B) vector efficiently delivered and expressed the *stv-a* and *stva-mIgG* genes in all tissues tested, and resulted in a significant antiviral effect on ALV(A) infection and replication. By delivering

the *stva* genes in the early embryo, the immune system of the chicken can be evaded. The birds are tolerized to the sTva and sTva-mIgG proteins, and to most of the ALV antigens since the viral vector used to deliver *stva* and *stva-mIgG* and the challenge viruses are virtually identical except for small regions of SU. The expression of the sTva and sTva-mIgG proteins *in vivo* allowed the examination of the effects of the viral glycoprotein-soluble receptor interactions in a wide variety of cells. One RAV-1 challenged RCASBP(B)stva infected bird did contain infectious ALV(A) in its serum. Unfortunately the bird died of non-viral causes before tissues could be obtained.

CD4, an important cell-surface protein of the T-lymphocytes, is the primary receptor for HIV-1. Several groups developed and expressed soluble forms of CD4 (sCD4) and demonstrated that recombinant sCD4 proteins could bind specifically to HIV-1 envelope glycoproteins and inhibit HIV-1 infection *in vitro* (Daar et al., 1990; Harbison et al., 1990; Klasse et al., 1993; Orloff et al., 1993; Schacker et al., 1995; Weiss, 1992). For injection of a recombinant antiviral protein to be effective against cell to cell transmission of the virus, it may be necessary to use a gene therapy approach in which target cells actively express the soluble receptor. The gene therapy approach has been tested for HIV-1: a sCD4 gene construct was expressed by a murine leukemia virus-based retroviral vector in human T-cell lines and in primary peripheral blood lymphocytes (Morgan et al., 1994). In cell culture populations engineered to express sCD4 (30-50% of the cells contained the sCD4 gene) HIV-1 replication was inhibited 50-70% indicating that a sCD4 antiviral approach against HIV-1 might be more effective. Since the initial sCD4 studies were published, the chemokine receptors have been identified as co-receptors necessary for efficient HIV-1 entry into cells (Hunter, 1997). Since both CD4 and a chemokine receptor are required for efficient HIV-1 entry into cells, sCD4 alone may not be an effective inhibitor of HIV-1 entry.

The results clearly indicate that a soluble receptor interference antiviral strategy can effectively block the replication of at least some retroviruses, and that this approach may be applicable to other virus groups that require specific viral glycoprotein-host receptor interactions for entry into the cell. The application of this strategy to protect animals against specific viral diseases is

relatively straightforward since transgenic technology can be used to introduce genes into animals and the transgenes will produce the desired protein without provoking an immune response.

Example 6

Selection of Subgroup A Avian Leukosis Virus Mutants Resistant to the Receptor Interference Imposed by Soluble TVA and SUA

Genes encoding soluble forms of the subgroup A avian leukosis virus (ALV) receptor Tva (sTva) and soluble envelope surface glycoprotein (SUA), delivered by ALV-based retroviral vectors to cells, significantly inhibit ALV(A) infection of those cells. The antiviral effects of sTva and SUA are consistent with a receptor interference (RI) mechanism; the antiviral effect is specific for ALV(A) since the susceptibility to infection by a neutral subgroup remains unchanged. A virus-free stable cell line was developed which expressed either sTva or SUA and so was significantly resistant to ALV(A) infection, 50-350-fold and 1,000 to 200,000-fold, respectively. Since the SU region of Env determines receptor usage, mutations capable of overcoming the RI may occur in the SU region of the *env* gene of ALV(A) and would affect interactions between Tva and Env(A).

ALV(A) was passaged on the sTva and SUA expressing cell lines. Variant viruses capable of more rapid growth on the sTva cell lines were identified at passage 7 and on the SUA cell lines at passage 9 post-infection. The SU region of the *env* gene was PCR amplified from these cells, cloned and analyzed by sequencing. Selection on sTva expressing cells produced mutant viruses which were identical in sequence to ALV(A) except that 50% of the clones screened had an amino acid change at codon 142, while the other 50% had an amino acid change at codon 149 of *env*. All mutants selected on SUA expressing cell lines contained a 6 amino acid deletion at codons 155-160 within *env*. To determine if these mutations were sufficient to confer enhanced growth on the resistant cell lines, the SU region of *env* containing the mutation, from Kpn I to Sal I, was introduced into a wild-type ALV(A) molecular clone.

Transfection of these mutants showed an enhanced rate of growth as compared to wild-type.

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All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the detailed herein may be varied considerably without departing from the basic principles of the invention.